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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

US-09-765-739A-2 110 1 NTTTGVFGLKQDWDGATIKD 20 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

1.00059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	squa	Q03263 saccharomyc	Q27483 caenorhabdi		P37197 escherichia	_	4		8 bacil				7				027139 methanobact			escheri	P79775 gallus gall				007934 bacillus su	_		025956 helicobacte	_	-	bacillus	1627 caprin	Pubbbb rattus norv
SUMMARIES	ID	NKC1_SQUAC	YM8M_YEAST	K6PF_CAEEL	YQAK_BACSU	YHJA_ECOLI	VP3_в РРН6	ATNA_ARTSF	AROE_SYNY3	PYRC_BACCL	ATN1_CANFA	YJJW_ECOLI	YM16_MYCLE	DNAA_STRCO	ATN2_HUMAN	GCST_NEIMB	GCST_NEIMA	YA67_METTH	KIME_RAT	VP4_ROTGA	YCBS_ECOLI	ANF1_CHICK	PURL_ZYMMO	DPYD_HUMAN	GVM1_HALN1	YRAJ_BACSU	PGHD_URSAR	BIOB_HELPJ	BIOB_HELPY	Y33B_MYCPN	UBPT_CAEEL	AMPA_BACSU	ENV_CAEVG	ATNZ_RAT
	Length DB		540 1	26	84		648 1		290 1				307 1								,	196									68	500 1	~ .	T 070T
de	Query	6.	N	ö	ö	。		40.0	39.5	39.1	39.1	38.2	38.2	38.2	38.2	37.7	37.7	37.3	37.3	37.3	37.3	36.8	36.8	36.8	36.4	36.4	36.4	36.4	36.4	36.4	36.4	36.4	36.4	
	Score		47	45	44	44	44	4	43.5	43	43	42	42	42	-	41.5		41	41	41		40.5			40	40	40	40	40	40	40	40	40	*
	Result No.	-	7	m	4	2	9	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	. m	

P05023 homo sapien	P13607 drosophila	P55012 mus musculu	P55011 homo sapien	P13508 caenorhabdi	P14585 caenorhabdi	P24620 micromonosp	P40756 rana catesb	P24021 aspergillus	P57922 pasteurella	P81989 cellulomona	Q02278 mycobacteri	
ATN1_HUMAN	ATNA_DROME	NKC1_MOUSE	NKC1_HUMAN	GLP1_CAEEL	LI12_CAEEL	YGRM_MICEC	ANFD_RANCA	NUS1_ASPOR	APAH_PASMU	PUNA_CELSP	YMA2_MYCBO	
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1023	1041	1205	1212	1295	1429	105	118	267	275	282	298	
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36	36	36	36	36	36	35	35	35	35	35	35	
40	40	40	40	40	40	39	39	39	39	39	39	
34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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us-09-765-739a-2.rsp

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                                                                                                                                                                                                                                                                            256 NVPTNIHGLSMDWTGSAL 273
190
2524
2524
253
316
316
316
316
410
410
410
410
52
52
11
                                                                                                                                                                                                                                                          1 NTTTGVFGLKQDWDGATI 18
                                                                                                                                                                                                   Query Match
Best Local Similarity 38.9
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VFGLKQDWDGATIKD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                           (PHOSPHOHEXOKINASE).
                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
 170
204
233
233
2273
2273
335
373
373
430
430
462
503
                                                                                                                                                                                                                                                                                                                                                        K6PF_CAEEL
027483;
 TRANSMEM
                                                                                                                                                                                                                                                                                                                              RESULT 3
K6PF_CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAINS-28BC / AB972;
STRAINS-28BC / AB972;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ datebases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROFEIN (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN AS THE DRUG RESISTANCE TRANSLOCASE FAMILY). DHA12 SUBFAMILY.
STRONG, TO YEAST ATRI.
                                                                                                                                                                                                                                                                     (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyceteles;
Saccharomyceteles; Saccharomycetaceae; Saccharomyces.
NCBL_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HYPOTHETICAL 59.6 KDA PROTEIN IN DSK2-CAT8 INTERGENIC REGION.
WMR279C OR YM8021.05C.
                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 1191;
         CYTOPLASMIC (POTENTIAL).
POTENTIAL.
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
POTENTIAL.
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CYTOPLASMIC (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POLY-PRASMIC (POTENTIAL).
POLY-CALY.
POLY-CALY.
POLY-ALA.
POLY-BO.

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                                                                                                                                                                                                                                                                                                                              PHOSPHORYLATION.
W; BA7BB9815431500C CRC64;
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POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          540 AA.
                                                                                                                                                                                                                                                                                                                                                                                   Score 51; DB Pred. No. 2; 2; Mismatches
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Best Local Similarity 58.8%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                         129774
                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 TGVFGLKQDWDGATIKD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                             546
189
1114
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Hypothetical protein; T
TRANSMEM 62 82
TRANSMEM 109 129
TRANSMEM 132 152
 82
129
152
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                                                                                                                                                                                                                                                                                                                                           AA;
 YM8M_YEAST
Q03263;
                                                                                                                                                                                                                                                                  CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                               MOD_RES
MOD_RES
SEQUENCE
                            TRANSMEM
DOMAIN
TRANSMEM
                                                                                  TRANSMEM
                                                                                                                            RANSMEM
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                                                                                                                                                                                                                                                                                                  CARBOHYD
 TRANSMEN
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YM8M_YEAST
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                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE 6-PHOSPHOFRUCTOKINASE (EC 2.7.1.11) (PHOSPHOFRUCTOKINASE)
                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                 Length 540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 756;
                                                                                                                                                                                                                                                                                                                                                                            8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
POTENTIAL.
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WormPep, C50Fd-2; CE0540-6.

InterPro; IRFO00002; Phosphofructokinase.

PRINTS; PRO0476; PHFKTKINASE.

PRODM; PRO04707; Phosphofructokinase; 2.

PROSTE, PSO0433; PHOSPHOFRUCTOKINASE; 1.

Kinase; Trafferase; Glycolysis; Repeat.

SEQUENCE 756 AA; 83301 MW; 26A89B801D286534 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 9
                                                                                                                                                                                                                                                                                                                              Score 47; DB 1;
Pred. No. 3.9;
3; Mismatches
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40.9%; Score 45; DB 1;
Best Local Similarity 53.3%; Pred: No. 12;
Matches 8; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   756 AA.
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YQAK_BACSU

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HEME 1 (COVALENT) (BY SIMILARITY).
HEME 1 (COVALENT) (BY SIMILARITY).
IRON 1 (HEME PROXIMAL) (BY SIMILARITY).
HEME 2 (COVALENT) (BY SIMILARITY).
HEME 2 (COVALENT) (BY SIMILARITY).
HEME 3 (COVALENT) (BY SIMILARITY).
HEME 3 (COVALENT) (BY SIMILARITY).
HEME 3 (COVALENT) (BY SIMILARITY).
IRON 3 (HEME PROXIMAL) (BY SIMILARITY).
IRON 3 (HEME DISTAL) (BY SIMILARITY).
IRON 3 (HEME DISTAL) (BY SIMILARITY).
                                                                                                                                                   STRAIN=KI2 / MG1655;
STRAIN=KI2 / MG1655;
STRAIN=KI2 / MG1655;
STRAIN=KI2 / MG1655;
SOTIA H.3.
SOTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gottlieb P., Metzger S., Romantschuk M., Carton J., Strassman J.,
Bamford D.H., Kalkkinen N., Mindich L.;
                                 Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 1; Length 465;
Pred. No. 10;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EcoGene; EG12244; YhjA.
InterPro; IPR000345; CytC_heme_bind.
InterPro; IPR003088; Cyt_CI.
Pfam; PF00034; cytochrome_c: 1.
PROSITE; PS00190; CYTOCHROME_C; 3.
Hypothetical protein; Oxidoreductase; Peroxidase; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p3.
Bacteriophage phi-6.
Virnses; dsRNA_viruses; Cystoviridae; Cystovirus
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01-JUL-1989 (Rel. 11, Last sequence update)
01-JAN-1990 (Rel. 13, Last annotation update)
P3 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           648 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Electron transport; Complete proteome.
BINDING 59 59 HEME 1 (C
BINDING 62 62 HEME 1 (C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE000428; AAC76543.1; -.
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52.9%;
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243 VENVEQFWDGRAATLQD 259
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Best Local Similarity 52.5.
The Conservative
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62
2010
2010
3354
429
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63
207
210
211
351
354
355
429
465 AA;
Escherichia coli
                                                                                              NCBI_TaxID=562;
                                 Bacteria; Pr
Escherichia
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P11129;
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BINDING
BINDING
METAL
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MEDLINE=96084975; PubMed=7489895;
Medigue C., Moszer I., Viari A., Danchin A.;
"Analysis of a Bacillus subtilis genome fragment using a co-operative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sato
                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 32.2 KDA PROTEIN IN SPOIIIC-CWLA INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-168 / JH642;
MEDLINE-95219086; Pubbed=7704261;
Takemaru K.-I., Mizuno M., Sato T., Takeuchi M., Kobayashi Y.;
Takemaru E.-I., Mizuno M., Sato T., Takeuchi M., Kobayashi Y.;
Takemaru K.-I., Mizuno M., Sato T., Takeuchi M., Kobayashi Y.;
Takemaru K.-I., Mizuno M., Sato T., Takeuchi M., Kobayashi Y.;
Takemaru H. Janan Mizuno M., Sato T., Takeuchi M., Kobayashi Y.;

Takemaru H., Mizuno M., Sato T., Takeuchi M., Kobayashi Y.;

Takemaru H., Mizuno M., Sato T., Takeuchi M., Kobayashi Y.;

Takemaru M., Mizuno M., Sato T., Takeuchi M., Kobayashi Y.;

Takemaru M., Sato T., Takeuchi M., Kobayashi Y.;

Takeuchi M., Sato T., Takeuchi M., Kobayashi Y.;

Takeuchi M., Sato T., Takeuchi M., Kobayashi Y.;

Takeuchi M., Sato T., Takeuchi M., Kobayashi M., Sato M., Sa
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0
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Kobayashi Y., Mizuno M., Masuda S., Takemaru K., Hosono S.,
Takeuchi M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 284;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ); Complete proteome.
32170 MW; F255261D4692ADB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
20-NUG-2001 (Rel. 40, Last annotation update)
YHJA OR B3518.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44; DB J
Pred. No. 6.1;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       465 AA.
                                                                                                                                                                                            284 AA
                                                                                                                                                                                                                                                            Created)
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53.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      computer system prototype.";
Gene 165:GC37-GC51(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 40.0
Best Local Similarity 53.8
Matches 7; Conservative
436 VIGIKHGWDGLKNKD 450
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                                                                                                                                                                                            STANDARD:
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                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, 01-NOV-1995 (Rel. 32, 20-AUG-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 FGLKQDWDGATIK 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical
SEQUENCE 28
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ID YHJA_ECOLI
AC P37197;
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P45908;
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AROE_SYNY3
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                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE FROM N.A.

MEDLINE-920390312; PubMed=1657719;

MEDLINE-920390312; PubMed=1657719;

MEDLINE-920390312; PubMed=1657719;

"Cloning of a cDNA encoding an Artemia franciscana Na/K ATPase alpha-
subunit.";

"Gene 105:197-204(1991).

"FORWING THIS IS THE CATALYTIC COMPONENT OF THE ACTIVE ENZYME,
"HACH CATALYZES THE HYDROLYSIS OF ATP COUPLED WITH THE EXCHANGE OF
NA & K IONS ACROSS THE PLASMA MEMBRANE. THIS ACTION CREATES THE
ELECTROCHEMICAL GRADIENT OF NA & K, PROVIDING THE ENERGY FOR
ACTIVE TRANSPORT OF VARROUS NUTRIENTS.

"CATALYTE CACTIVITY: ATP + H(2)O + H(+)(IN) + NA(+)(OUT) = ADP +
PHOSPHART ENERGY FOR THREE SUBUNITS: ALPHA (CATALYTIC), BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATNA_ARTSF STANDARD; PRT; 1004 AA.
P28774;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SODIUM/POTASSIUM-TRANSPORFING ATPASE ALPHA CHAIN (EC 3.6.3.9) (SODIUM
"Nucleotide sequence of the middle dsRNA segment of bacteriophage phi 6: placement of the genes of membrane-associated proteins."; Virology 163:183-190(1988).

-i. FUNCTION: P3 PROTEIN IS NECESSARY FOR ADSORPTION ONTO HOST
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUMP) (NA+/K+ ATPASE).
Artemia sanfranciscana (Brine shrimp) (Artemia franciscana).
Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;
Artemidae; Artemia.
                                                                                                                                                                                                                                                                                                                                                                                    5
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                                                                                                                                                                                                                                                                                                                                               Score 44; DB 1; Length 648;
Pred. No. 15;
5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                 648 AA; 69178 MW; B188DFE02ACC54E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, X56650; CAA39972.1; -.
PIR, JH0470; JH0470.
InterPro; IPR001757; E1-E2_ATPase.
                                                                                                                                                                                                                                                                                                                                                                                    . .
                                                                                                                                                                                                                                          EMBL; M17462; AAA68485.1; -. PIR; C28648; P3BPF6. Envelope protein. SEQUENCE 648 AA; 69178 MW;
                                                                                                                                                                                                                                                                                                                                                   40.08;
llarity 41.28;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        :|| :| ||:|: |
181 IFGWYVKMDWEGSAVAD 197
                                                                                                                                                                                                                                                                                                                                                                                                                      6 VFG--LKQDWDGATIKD 20
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                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Kaneko T., Sato S., Rotani H., Sugiura M., Sasamoto S., Kimura T.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PATHWAY: FOURTH STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- CATALYTIC ACTIVITY: SHIKIMATE + NADP(+) = 5-DEHYDROSHIKIMATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44; DB 1; Length 1004;
Pred. No. 24;
1; Mismatches 5; Indels
                                                                                                                                                                                                           BY SIMILARITY.
POSCHORYLATION (PROBABLE).
ATP (BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY).
CE4E6BECE19A78C7 CRC64;
                 InterPro; IPR000661; Na_H_K_ATPase.
Pfam, PF00122; B1-E2_ArPase; 1.
Pfam; PF00702; Hydrolase; 1.
Pfam; PF00689; Na_K_ATPase_C; 1.
Pfam; PF00689; Na_K_ATPase_N; 1.
PRINTS; PR00119; CATATPASE_N; 1.
PRINTS; PR00119; CATATPASE_N; 1.
PRINTS; PR001154; ATPASE_E_E_E; 1.
PHYGROLASE; Sodium/potassium transport; Transmembrane; Phydrolase; Sodium/potassium transport; Transmembrane; Phydrolase; ATPASE_E_E_E_E, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACOE_SYNY3 STANDARD; PRT; 290 AA. P74591; 200 AA. D74591; 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) ARCE OR SLR1559.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D90916; BAA18699.1; -.
InterPro; IPR002907; Shikimate_DH.
InterPro; IPR001454; Hydrolase.
InterPro; IPR000661; Na_H_K_ATF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       110699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 VFGLKQDWDGATIKD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
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Best Local Similarity
دعد 6; Conser
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TRANSMEM
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ATN1_CANFA
P50997;
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                                                 ATN1_CANFA
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                                                                                                                              1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \operatorname{Ghim} S.Y., Nielsen P., Neuhard J.; "Molecular characterization of pyrimidine blosynthesis genes from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WHICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- COFACTOR: THIS ENZYME TIGHTLY BINDS ONE ZINC ATOM PER CHAIN WH
IS REQUIRED FOR THE CATALYTIC MECHANISM. IT ALSO BINDS WEAKLY
TWO OTHERS ZINCS WHICH ARE NOT ESSENTIAL FOR ACTIVITY
(BY SIMILARITY).
                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thermophile Bacillus caldolyticus.";
Microbiology 140:479-491(1994).
-i- CATALYTIC ACTIVITY: DIHYDROOROTATE + H(2)0 = N-CARBAMOYL-
                                                                                               Length 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY).
---- PATHAAY: THIRD STEP IN PYRIMIDINE BIOSYNTHESIS.
---- SUBUNIT: HOMODIMER (BY SIMILARITY).
---- SIMILARITY: BELONGS TO THE DHOASE FAMILY. SUBFAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 427;
                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
Pfam; PF01488; Shikimate_DH; 1.
Aromatic amino acid biosynthesis; Oxidoreductase; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          759A2AA99F733F4E CRC64;
                                                 31099 MW; 8A2D38EE5D57B303 CRC64;
                                                                                                                            5,
                                                                                                                                                                                                                                                                                                                                                                                 Bacillus caldolyticus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                               DB 1;
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Pred. No. 14;
0; Mismatches
                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DIHYDROOROTASE (EC 3.5.2.3) (DHOASE).
                                                                                                                                                                                                                                                                        427 AA
                                                                                             Score 43.5; D
Pred. No. 7.6;
                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002195; Dihydrocratase.
Pfam; PF00744; Dihydrocratase; 1.
PROSITE; PS00482; DIHYDROOROTASE_1; 1.
PROSITE; PS00483; DIHYDROOROTASE_2; 1.
PyrImidine biosynthesis; Hydrolase; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus/Staphylococcus group; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=DSM 405;
MEDLINE=94282293; PubMed=7516791;
                                                                                                                                                                                           105 INTDVEGFLAPLLELKQDWSGRT 127
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68.8%;
                                                                                             39.5%;
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                                                                                             Query Match 39.55
Best Local Similarity 47.89
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
                                                                                                                                                                                                                                                                        STANDARD;
                                               290 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                  Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1394;
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                                                                                                                                                                                                                                                                       PYRC_BACCL
P46538;
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                                                 SEQUENCE
                                                                                                                                                                                                                                                        PYRC_BACCL
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4 TGVFGLKQDWDGATIK 19

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canassa C.M., Horisberger J.D., Louvard D., Rossier B.C.;
"Mutation of a cysteine in the first transmembrane segment of Na,K-
ATPASe alpha subunit confers ouabain resistance.";
EMBO J. 11:1681-1687(1992).
-!- FUNCTION: THIS IS THE CATALYTIC COMPONENT OF THE ACTIVE ENZYME,
WHACH CATALYZES THE HYRROLYSIS OF ATP COUPLED WITH THE EXCRANGE OF
NA & K IONS ACROSS THE PLASMA MEMBRANE. THIS ACTION CREATES THE
ELECTROCHEMICAL GRADIENT OF NA, E, PROVIDING THE ENERGY FOR
ACTIVE TRANSPORT OF VARIOUS NUTRIENTS.
-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(IN) + NA(+)(OUT) = ADP +
PHOSPHATE + H(+)(OUT) + NA(+)(IN).
-!- SUBUNIT: COMPOSED OF THREE SUBUNITS: ALPHA (CATALYTIC), BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SODIUM/POTASSIUM-TRANSPORTING ATPASE ALPHA-1 CHAIN.
                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Xie Z., Li H., Liu G., Wang Y., Askari A., Mercer R.W.;
"Cloning of the dog Na/K-ATPase alpha 1 subunit.";
(In) Bamberg E., Schoner W. (eds.);
The sodium pump, pp.49-52, Springer-Verlag, New York (1994).
                                                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SODIWA/POTASSIUM-TRANSPORTING ATPASE ALPHA-1 CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00154; ATPASE_EL_E2; 1.
Hydrolase; Sodium/potassium transport; Transmembrane;
Multigene family; Phosphorylation; ATP-binding.
1021 AA
                                                                                                                                                                                         (EC 3.6.3.9) (SODIUM PUMP) (NA+/K+ ATPASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LITERPROS I PRO01757; E1-E2_ATPASE.
INTERPRO; IPR001557; E1-E2_ATPASE.
INTERPRO; IPR001654; Hydrolase.
INTERPRO; IPR001651; NA_HK_ATPASE.
Pfam; PF00122; E1-E2_ATPASE; I.
Pfam; PF00699; NA_K_ATPASE, I.
Pfam; PF00699; NA_K_ATPASE_C; I.
Pfam; PF00699; NA_K_ATPASE_C; I.
PRINTS; PR00119; CATATPASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Kidney;
MEDLINE=92258376; PubMed=1316269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE OF 92-307 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L42173; AAA67372.1; -. EMBL; X66174; CAA46950.1; -.
   STANDARD;
                                                                                                                                                                                                                                                        Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1021
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Best Local Similarity 50...
8; Conservative
... 8; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                              GVFGLKQDWDGATIKD 20
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143 LCQDWEGATL 152
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032960;
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YM16_MYCLE
1D 729560
DT 30-MAY
DA MYCODA
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Nucleic Acids Res. 23:2105-2119(1995).
-!- COFACTOR: BINDS A 4FE-4S CLUSTER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VJJW OR B4379.
Escherichia coli.
Bacteriaj Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAMILY.
-:- SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE OF
'BACTERIAL-TYPE' 4FE-4S FERREDOXINS.
                                                                                                                                                                                                                                                                                                                                                              ó
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01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 40, Last annotation update)
HYPOTHETICAL 31.5 KDA PROTEIN IN OSMY-DEOC INTERGENIC REGION
                                                                                                                                                                                                                                                                                                      Score 43; DB 1; Length 1021;
Pred. No. 36;
2; Mismatches 7; Indels
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
PHOSPHORYLATION (PROBABLE).
ATP (BX SINTLARITY).
C -> Y (IN REF. 2).
I -> V (IN REF. 2).
K -> E (IN REF. 2).
L -> F (IN REF. 2).
L -> F (IN REF. 2).
C -> F (IN REF. 2).
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STRAIN=K12 / MG1655;
MEDLINE=95334362; Pubmed=7610040;
Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         287 AA.
                                                                                                                                                                                                                                                                                                         Query Match 39.1%;
Best Local Similarity 47.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                      112666
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P39409;
  TRANSMEM
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        SOTETT
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Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
1- SIMILARITY: BELONGS TO THE UPF0105 FAMILY.
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STRAIN=TN.
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STRAIN=TN.
STRAIN=TN.
COLE S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Whungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Ollver K., Quall M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39; Last amotation update)
20-AUG-2001 (Rel. 40, Last amotation update)
HYPOTHERICAL 32.9 KDA PROTEIN ML0860.
ML0860 OR MLCB22.1 Mycobacterium leprae.
Bacteria, Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBL_TAXID=1769;
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IRON-SULEUR I (4FE-45) (BY SI
IRON-SULEUR I (4FE-5) (BY SI
IRON-SULEUR 2 (4FE-45) (BY SI
4) EORBB429519E54B3 CRC64;
                                                                                                                                                                                                                                                                                                                                              6; Indels
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EMBL; AL583920; CAC31241.1; -.
Leproma; MLO860; -.
Hypothemical protein; Complete proteome.
SEQUENCE 307 AA; 32853 MW; EEFESBA102455DA2 CRC64;
                                                                                                                                                                                                                                                                                       Score 42; DB 1;
Pred. No. 13;
; Mismatches
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Pred. No. 14;
2; Mismatches
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30-MAY-2000 (Rel. 39, Last seq
                                                                                                                                                                                                    MM;
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70.0%;
                                                                                                                                                                                                                                                                                   38.2%;
50.0%;
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us-09-765-739a-2.rsp

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EC 3.6.1.37) (SODIUM PUMP) (NA+/K+ ATPASE)
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                                                                                                                                                                                                                              Calcutt M.J., Schmidt F.J.; "Conserved gene arrangement in the origin region of the Streptomyces coelicolor chromosome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                            Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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01-ocT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SODIUM/POTASSIUM-TRANSPORTING ATPASE ALPHA-2 CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.2%; Score 42; DB 1; Length 656; 36.8%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Indels
                                                                                       Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NA replication; DNA-binding; ATP-binding.
NP_BIND 357 364 ATP (POTENTIAL).
SEQUENCE 656 AA; 73182 MW; 6C1D5C0193D3C92B CRC64;
                DNAA_STRCO STANDARD; PRT; 656 AA. P27902; O9KXX4; 01-AUG-1992 (Rel. 23, Created) 01-AUG-1992 (Rel. 23, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) CHROWOSOMAL REPLICATION INITIATOR PROTEIN DNAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1020 AA.
                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE DNAA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Mismatches
                                                                                                                                                                                                   Bacteriol. 174:3220-3226(1992).
                                                                                                                                                  STRAIN=A3(2);
MEDLINE=92250416; PubMed=1577691;
                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AF187159; AAA26734.1; -. BMBL, A1357152; CAB92999.1; -. PIR, A41870; A41870. InterPro; IPR003593; AAA. InterPro; IPR001997; Bac_DnaA. Pfam; PF00308; bac_dnaA; 1. PRINTS; PR00051; DNAA.
                                                                                                                                                                                                                      SEQUENCE OF 51-656 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:| : | | |:| |::| 563 TSTAIMGATADYFGLTVED 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 TTTGVFGLKQDWDGATIKD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00382; AAA; 1.
PROSITE; PS01008; DNAA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                        SEQUENCE FROM N.A.
                                                                              DNAA OR SCH18.16C.
                                                                                                                      NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATN2_HUMAN
P50993;
01-OCT-1996 (
01-OCT-1996 (
20-AUG-2001 (
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Matches
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ATN2_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISGUE-Placenta, and Brain;

X MEDLINE=8724723; PubMed-3036582;

X MEDLINE=8724723; PubMed-3036582;

X MEDLINE=8724723; PubMed-3036582;

X Allikmets R.L., Melkov A.M., Smirnov Y.V., Malyahev I.V.,

Allikmets R.L., Melkov A.M., Smirnov Y.V., Malyahev I.V.,

X Dulobova I.E., Petrukhin K.E., Grishin A.V., Kijatkin N.I.,

X Kostina M.B., Sverdlov V.E., Modyanov N.N., Ovchnikov Y.A.;

Y The family of human Na+ K+ -ATPase genes: NO less than five genes

XT The family of human Na+ K+ -ATPase genes: NO less than five genes

XT The family of human Na+ K+ -ATPase genes: NO less than five genes

XT THE CANTION: THIS IS THE CANTALYTIC COMPONENT OF THE ACTIVE ENZYME,

XI INS ACROSS THE PLASMA MEMBRANE. THIS ACTION CREATES THE

ELECTROCHEMICAL GRADIENT OF NA E. K, PROVIDING THE ENERGY FOR

ACTIVE TRANSFORT OF VARIOUS NUTRIENTS.

C -1- CATALYTIC ACTIVITY: ATP + H(-2)O + H(+)(IN) + NA(+)(OUT) = ADP +

PHOSPHARE + H(+)(OUT) + NA(+)(IN).

C -1- SUBUNITS: CANTALYTIC), BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND GAMMA.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- HISCELLANEOUS: THE ALPHA SUBUNIT IS ENCODED BY A WULTIGENE FAMILY.
-!- MISCELLANEOUS: THE ALPHA SUBUNIT MAY HAVE SPECIALIZED FUNCTIONS.
-!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Multiple genes encode the human Na+,K+-ATPase catalytic subunit.";
Proc. Natl. Acad. Sci. U.S.A. 84:4039-4043(1987).
                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                        MEDLINE=90008924; PubMed=2477373;
Shull M.M., Pugh D.G., Lingrel J.B.;
"Characterization of the human Na,K-ATPase alpha 2 gene and identification of intragenic restriction fragment length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Sodium/potassium transport; Transmembrane; Multigene family; Phosphorylation; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001757; E1-E2_ATPase.
InterPro; IPR001454; Hydrolase.
InterPro; IPR000661; Na_M_K_ATPase.
Pfam; PF00122; E1-E2_ATPase; 1.
Pfam; PF00702; Hydrolase; 1.
Pfam; PF00689; Na_K_ATPase_C; 1.
Pfam; PF00689; Na_K_ATPase_C; 1.
PRINTS; PR00119; CATATPASE.
PRINTS; PR001121; NNKATPASE.
PROSITE; PS00154; ATPASE_E1_E2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol. Chem. 264:17532-17543(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Leukocyte;
MEDLINE=87231946; PubMed=3035563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M27578; AAA35575.1;
EMBL; M27571; AAA35575.1; JOINED.
EMBL; M27576; AAA35575.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 251-442 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 211-249 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; J05096; AAA51797.1; -. EMBL; M16795; AAA51799.1; -. EMBL; M27578; AAA35575.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shull M.M., Lingrel J.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (E1-E2 ATPASES).
    (Human)
                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                    polymorphisms.";
                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 182340; -
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-MCS8 / SERGGROUP B;
STRAIN-MCS8 / SERGGROUP B;
STRAIN-MCS8 / SERGGROUP B;
STRAIN-E-201755; PubMed=10710307;
Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
Eisen J.A., Retchum K.A., DeBoy R., Peterson J.D., Hickey E.K.,
Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
Mason T. Clecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,
Gotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
Glill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,
Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
"Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE AMINOMETHYLTRANSFERASE (EC 2.1.2.10) (GLYCINE CLEAVAGE SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=491;
BY SIMILARITY.
SODIOW/POTASSIUM-TRANSPORTING ATPASE
ALPHA-2 CHAIN.
POTENTIAL.
POSSHORVALATION (PROBABLE).
ATP (BY SIMILARITY).
5 MW; AFBDBEA94FFB4FC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
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Pred. No. 53;
4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      366 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE002413; AAF41002.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                           38.2%;
                                                                                                                                                                                                                                                                                                                                     112265
                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 40.(
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : |:: ||| |: |
880 LLGIRLDWDDRTMND 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 VFGLKQDWDGATIKD 20
                                                                              94 111
289 314
289 318
318 34
784 86
8146 87
913 93
950 97
950 97
950 87
1020 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCVT OR NMB0574.
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                                                                                                                                                          TRANSMEM
TRANSMEM
TRANSMEM
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MOD_RES
BINDING
SEQUENCE
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FRANSMEM
                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCST_NEIMB
        Db
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InterPro; IPR002536; GCV_T

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5
                                                                                                                                   Gaps
                                                                                                                                 11;
                                                                                             DB 1; Length 366;
                                                                                                                                 Indels
Pfam; PF01571; GCV_T; 1.
Transferase; Aminotransferase; Complete proteome.
SEQUENCE 366 AA; 39740 MW; 566A7BCD21691D91 CRC64;
                                                                                         Query Match 37.7%; Score 41.5; D
Best Local Similarity 44.8%; Pred. No. 21;
Matches 13; Conservative 2; Mismatches
                                                                                                                                                                                      2 TTTGVF--GLKQ------DWDGATIK 19
                                                                                                                                                                     ò
                                                                                                                                                                                                   Db
```

Search completed: March 14, 2002, 09:24:49 Job time: 905 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

March 14, 2002, 09:10:41; Search time 56.96 Seconds (without alignments) 26.747 Million cell updates/sec

US-09-765-739A-2

110 1 NTTTGVFGLKQDWDGATIKD 20 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		dР				
Result		Query				
No.	Score	Match	Length	DB	ID	Description
1 1 1 1		1 1 1 1 1		:		
П	90	81.8	280	7	JE0217	surface
7	82	74.5	276	7	JE0218	28k surface antige
က	71	64.5	286	7	JE0219	28k surface antige
	59	53.6	278	7	JE0216	28k surface antige
5	59	53.6	284	7	I40882	ige
9	52	47.3	5188	7	B85547	probable RTX famil
7	51	46.4	1191	7	A53491	e-s
œ	49	44.5	133	7	JE0221	28k surface antige
Œ	47	42.7	540	~	S54586	probable membrane
10:	47	42.7	584	7	C48658	flagellin - Escher
11	46.5	42.3	267	7	C83242	conserved hypothet
12	46	41.8	261	~	G84057	hypothetical prote
13	45	40.9	. 160	7	A75466	_
14	45	40.9	756	7	T20109	hypothetical prote
15	44	40.0	284	2	B69945	σ
16	44	40.0	465	Н	S47738	-
	44	40.0	465	~	G86024	cytochrome-c perox
18	44	40.0	534	7	C82096	aminoacyl-histidin
	44	40.0	648	, - 1	P3BPF6	P3 protein - phage
	44	40.0	1004	7	JH0470	han
	43.5	39.5	290	7	S76787	hypothetical prote
	43	39.1	280	7	D70976	hypothetical prote
	43	39.1	427	~	140167	ŝ
	43	39.1	470	7	JC4098	tetracycline 6-hyd
	43	39.1	482	7	G75483	probable leucyl am
	43	39.1	1037	7	A56594	Na+/K+-exchanging
27	43	39.1	1649	7	C86822	hypothetical prote
	42	38.2	224	7	C72390	hypothetical prote
29	42	38.2	. 287	Н	S56603	probable pyruvate

probable activatin	hypothetical prote	S-adenosylmethioni	conserved hypothet	dnaA protein - Str	hypothetical prote	Na+/K+-exchanging	conserved hypothet	sugar ABC transpor	glycine cleavage s	probable aminometh	hypothetical prote	, hypothetical prote	hypothetical prote	hypothetical prote	peptide ABC transp
D86137	T44893	F75379	T08297	A41870	T00492	A34474	B64549	A84110	A81183	G81919	T23091	B85637	E84885	A69997	A75381
71	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
287	307	362	413	959	725	1020	176	293	366	368	468	95	244	269	376
38.2	38.2	38.2	38.2	38.2	38.2	38.2	37.7	37.7	37.7	37.7	37.7	37.3	37.3	37.3	37.3
42	42	42	42	42	42	42	41.5	41.5	41.5	41.5	41.5	41	41	41	41
		۵.	_			. ~	37	_	_	_		42	_	44	

ALIGNMENTS

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JEGOLY.

28k surface antigen 4 - Ehrlichia chaffensis

28k surface antigen 4 - Ehrlichia chaffensis

28k surface antigen 5 - Ehrlichia chaffensis

C. Species: Ehrlichia chaffensis

C. Species: Ehrlichia chaffensis

C. Accession: JEGOLY

R. Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.

Biochem. Biophys. Res. Commun. 247, 636-643, 1998

A, Title: Molecular characterization of a 28kDa surface antigen gene family of the tri
A, Reference number: JEGOLS

A, Reference number: JEGOLS

A, Molecule type: DNA

A, Molecule type: DNA

A, Residues: 1-280 cRED>

A, Cross-references: GB:AF062761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 90; DB 2; Length 280;
Pred. No. 1.3e-06;
1; Mismatches 1; Indels
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Gaps ; 0 Query Match 81.8%; Best Local Similarity 88.9%; Matches 16; Conservative

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1 NTTTGVFGLKQDWDGATI 18 60 NTTIGVEGLKQDWDGSTI 77 δy Q

JEGOLBS
28k surface antigen 5 - Ehrlichia chaffensis
C; Species: Ehrlichia chaffensis
C; Species: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 17-Mar-1999
C; Accession: JEGOLB
R; Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Biochem: Biophys. Res. Commun. 247, 636-643, 1998
A; Title: Molecular characterization of a 28kDa surface antigen gene family of the tri
A; Meference. number: JEGOLB
A; Accession: JEGOLB
A; Molecule type: DNA
A; Residues: 1-276 < RED>
A; Cross-references: GB:AF062761

Gaps ó 74.5%; Score 82; DB 2; Length 276; 70.0%; Pred. No. 2.3e-05; ive 3; Mismatches 3; Indels Best Local Similarity 70.0 Matches 14; Conservative Query Match

; 0

1 NTTTGVFGLKQDWDGATIKD 20 ò

59 NTTVGVFGLKQNWDGSAISN 78 В ~

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probable RTX family exoprotein [imported] - Escherichia coli (strain 0157:H7)
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Sacession: B6547
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May liler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Mature 409, 529-533, 2001
A;Title: Genome sequence of enterchemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bumetanide-sensitive Na-K-Cl cotransporter - spiny dogfish
C;Species: Squalus acanthias (spiny dogfish)
C;Date: 03-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 02-Mar-2001
C;Accession: A53491
R;Vu, J.C.; Lytle, C. C; Zhu, T.T.; Payne, J.A.; Benz Jr., E.; Forbush III, B.
Proc. Natl. Acad. Sci. U.S.A. 91, 2201-2205, 1994
A;Title: Molecular cloning and functional expression of the bumetanide-sensitive Na-K
A;Réference number: A53491; MUID:94181560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JE0221
28k surface antigen 2 - Ehrlichia canis
28k surface antigen 2 - Ehrlichia canis
C;Species: Ehrlichia canis
C;Species: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 21-Jul:2000
C;Accession: JE021
C;Accession: JE021
E;Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R Biochem. Biophys. Res. Commun. 247, 636-643, 1998
A;Title: Molecular characterization of a 28kDa surface antigen gene family of the tri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA.
A;Residues: 1-5188 <-STO>
A;Residues: 1-5188 <-STO>
A;Cross-references: GB.AE005174; NID:g12513368; PIDN:AAG54838.1; GSPDB:GN00145; UWGP: A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics: 20615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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     Gaps
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A; Molecule types: mRNA
A; Molecule types: mRNA
A; Rosidues: 1-1191 <XUA>
A; Rosidues: 1-1191 <XUA>
A; Coss.references: GB: U05958; NID: 9454096; PIDN: AAB60617.1; PID: 9454097
C; Superfamily: rat bumetanide-sensitive Na+/K+/C1--cotransport protein
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46.4%; Score 51; DB 2; Length 1191;
Best Local Similarity 58.8%; Pred. No. 8.2;
Matches 10; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 5188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
     Indels
     5
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Pred. No. 28;
2; Mismatches
     Mismatches
     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 47.3
Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4803 TTSGVAAMDYDWDGA 4817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 TTTGVFGLKQDWDGA 16
                                                                                3 TTGVFGLKQDWDG 15
                                                                                                                                        63 TKAVFGLKKDWDG 75
10;
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                                                                                                                                                                                                                                                                                                         9
     Matches
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                                                            28K surface antigen 2 - Ehrlichia chaffensis
Nalternate names: MAP1
Nichternate names: MAP1
C; Species: Ehrlichia chaffensis
E; Spec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               major antigenic protein - heartwater rickettsia
C; Species: Cowdria ruminantium (heartwater rickettsia)
C; Species: Cowdria ruminantium (heartwater rickettsia)
C; Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 08-Oct-1999
C; Accession: 140882; A2827,
R; Van Vilet, A.H.; Jongejan, F.; van Kleef, M.; van der Zeijst, B.A.
Infect. Immun. 62, 1451-1456, 1994
A; Title: Molecular cloning, sequence analysis, and expression of the gene encoding the A; Reference number: 140882; MUID:94178956
A; Reference number: 140882
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-284 < RES>
A; Cross references: EMBL:X74250; NID:9454266; PIDN:CAA52309.1; PID:9454267
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Pred. No. 0.0013;
2; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 284;
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0.096;
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Pred. No. 0.094;
3; Mismatches
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Pred. No.
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66.7%;
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Best Local Similarity 66.7
Matches 12; Conservative
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Best Local Similarity 60.0
Matches 9; Conservative
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Best Local Similarity
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us-09-765-739a-2.rpr

C; Superfamily: flagellin

A; Reference number: JE0216; MUID: 98321180

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M.J.; K.; L

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A:Reference number: A82950; MUID:20437337
A;Accession: C83342
A;Accession: C83342
A;Accession: C83342
A;Actus: preliminary
A;Molecule type: DNA
A;Residues: 1-267 <STO>
A;Experimental source: GB:AE004746; GB:AE004091; NID:g9949350; PIDN:AAG06627.1; GSPDB:GN
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA3239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Species: Bacillus halodurans
C; pecies: Bacillus halodurans
C; pate. 01-pec-2000 #sequence_revision 01-pec-2000 #text_change 31-pec-2000
C; Accession: G84057
R; Takami, H; Nakasone, K:; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A; Reference number: A83650; MUID:20263314
                                                                                                                                                                                                                                                                                                                                                                                      conserved hypothetical protein PA3239 [imported] - Pseudomonas aeruginosa (strain PAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P.; Hickey,
A.; Larbig,
                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Pseudomonas aeruginosa
C;Bate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: C83242
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hick adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larb.; J. Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein BH3263 [imported] - Bacillus halodurans (strain C-125)
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                                                               Length 584;
                                                                                                                         Indels
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                                                         core 47; DB 2
red. No. 16;
Mismatches
                                                               Score 47;
Pred. No.
                                                                                                                         3;
                                                            42.7%;
ilarity 66.7%;
Conservative
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64.7%;
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Best Local Similarity 64.7
Matches 11; Conservative
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199 NTTTGLYGLKTE 210
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                                                            Query Match
Best Local Similarity
Matches 8; Conserv
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Matches 7; Conserv
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177 DWDGATVAD 185
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C;Superfamily:
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J. Bacteriol. 175, 5395-5402, 1993
A.Fitle: Comparative analysis of flagellin sequences from Escherichia coli strains posse
A.Reference number: A48658; MUID:93374833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-540 <PEA>
A;Residues: 1-540 <PEA>
A;Cross-references: EMBL:Z49704; NID:g825540; PIDN:CAA89777.1; PID:g825545; GSPDB:GN0001
A;Experimental source: strain AB972
C;Genetics:
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A;Accession: JE0221
A;Molecule type: DNA
A;Residues: 1-133 <RED>
A;Cross-references: GB:AF062762; NID:g3327964; PIDN:AAC26722.1; PID:g3327966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable membrane protein YMR279c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein YM8021.05c
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 05-Nov-1999
C;Accession: S54586
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C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 26-Aug-1999
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A;Cross-references: GB:L07388; NID:g290438; PIDN:AAA23798.1; PID:g290439
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Pred. No. 15;
                                                                                                                                                                                Length 133
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                                                                                                                                                                             DB 2;
1.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.Pearson, D.; Bowman, S. submitted to the EMBL Data Library, May 1995 A; Reference number: $54582 A; Accession: $54586
                                                                                                                                                                             Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            flagellin - Escherichia coli (strain U5-41)
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38.9%;
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56.2%;
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                                                                                                                                                                                                           Best_Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                 3 TTGVFGLKQDWDGATI 18
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: MIPS: YMR279c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accession: S54586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: 13R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;139-155/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;174-190/Domain:
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Nature 390, 249-256, 1997 'Analysis of Analysis of Analysis of Analysis Foulgar, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galisch, J.; Hardney, J.; Hardney, J.; Hardney, J.; Hardney, M.; Hardney, M.; Hardney, M.; Hardney, M.; Hardney, M.; Lapidus, A.; Liullo, M.; Analysis, M.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau Rieger, M.; Rivolta, C.; Rocha, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portere Analysis of Schleich, S.; Schleich, B.; Scoche, B.; Rose, M.; Sadoie, Y.; Sato, T.; Scanlakenth, M.; Tamancshi, A.; Tamanca, T.; Scolione, P.; Sekiguchi, J.; Sekwasa, A.; Se T.; Winters, P.; Wippt, A.; Tamancho, H.; Yamanca, K.; Yasumuto, N.; Tosato, V.; Orlyya A; Reference number: Action of Scolione Science of the Gram-positive bacterium Bacillus subtili A; Residues: Preliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-284 cKUN>
A; Residues: 1-284 cKUN>
A; Reseriamental source: Strain 168
Connection:
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Pred. No. 22;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: yqak
C;Superfamily: Escherichia coli recT protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: March 14, 2002, 09:10:42 Job time: 358 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 40.0%;
Best Local Similarity 53.8%;
Matches 7; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ωp
                                                  C. Species: Definococcus radiodurans
C. Species: Definococcus radiodurans
C. Species: Definococcus radiodurans
C. Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Sep-2000
C. Accession. A75466
R.White, O.: Bisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
A. Shan, M.; Vanathevan, J.G.; Fraser, C.M.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
A.Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A.Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A. Reference number: A75466
A. Status: preliminary
A. Molecule type: DNA
A. Residues: 1-160 <-MHI>
A. Kross-references: GB. AE001940; GB. AE000513; NID:g6458577; PIDN: AAF10437.1; PID:g645857
C. Generius:
A. Gene: DR0859
A. Map position: 1
C. Keywords: methyltransferase
                                       demethylmenaquinone 2-C-methyltransferase (EC 2.1.1.-) DR0859 [similarity] - Deinococo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pypothetical protein C50F4.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T20109
R;McMurzay, A.
S;McMurzay, A.
S;McMurzay, A.
S;McMurzay, A.
S;McMurzay, A.
S;McMurzay, T20109
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T20109
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: EMBL:270750; pIDN:CAA94737.1; GSPDB:GN00023; CESP:C50F4.2
A;Genetics:
C;Genetics:
A;Genetics:
A;Map position: 5
A;Map position: 5
A;Map position: 5
A;Introns: 2471; 245/3; 315/2; 389/3; 537/3; 568/2; 747/1
C;Superfamily: human 6-phosphofructokinase; 6-phosphofructokinase 1 homology
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8;
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40.9%; Score 45; DB 2; Length 756; Best Local Similarity 53.3%; Pred. No. 43; Matches 8; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45; DB
Pred. No. 8;
% Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 50.0%;
Matches 7; Conservative
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phage-related protein homolog yqak - Bacillus subtilis
C;Specias: Bacillus subtilis
C;Date: 05-Dec-1997 stext_change 20-Jun-2000
C;Date: 05-Dec-1997 steydence_revision 05-Dec-1997 #text_change 20-Jun-2000
R;Runst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S; Brouillet, S; Bruschi, C.V.; Caldwell, B; Capuano, V; Carter, N.M.; Chd
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J; Fabret, C; Ferrani, Chd

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Gaps · 0

Length 284; 5; Indels

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

March 14, 2002, 09:07:39; Search time 54.54 Seconds (without alignments) 8.252 Million cell updates/sec Run on:

US-09-765-739A-3 107 1 NTTVGVFGLKQNWDGSAISN 20 Perfect score:

Sednence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

212252 seqs, 22503292 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:* Database :

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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

COMMENTES	Length DB ID Description	276 4 US-08-953-326-18 Sequence 18, Appl	3 US-08-733-230-4 Sequence 4,	53-326-4	4 US-08-953-326-17 Sequence 17,	1-326-15 Sequence 15,	4 US-08-953-326-20 Sequence 20,	4 US-08-953-326-16 Sequence 16,	3 US-08-733-230-2 Sequence 2, A	4 US-08-953-326-2 Sequence 2,	3 US-08-840-146-19 Sequence 19,	3 US-09-360-220-19 Sequence 19,	2 US-08-436-771-11 Sequence 11,	00 2 US-08-434-998-11 Sequence 11,	2 US-08-487-797-11 Sequence 11,	5 PCT-US95-02058-11 Sequence 11,	2 US-08-630-822A-64 Sequence 64,	4 Sequence 64,	2 US-08-742-621-1 Sequence 1,	4 US-09-191-608-22 Sequence 2	1 US-08-462-484-10 Sequence 10	1 US-08-441-147-10 Sequence 10,	5 PCT-US95-07536-10 Sequence 1	2 US-08-276-967-2 Sequence 2, A	1 US-07-772-087-2	4 US-08-989-385-1 Sequence 1,	1 US-08-190-802A-70 Sequence 70,	
	, Length	1 1 1 1					.5	٠.	.7	.7	۳.	.3 365	.3 400	.3 400	3 400	3 400	137	137	388	388	527	527	527	4 2476	5 377	5 738	ص	
фP	Query Score Match	107 100.0	107 100	107 100.0		73	2		51 47	51 47	e		m	e	41 38			36 36.			6	6	S	σ	80		7	
	Result No.		2	e	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	

Sequence 173, App Sequence 70, Appl	173,	Sequence 41, Appl Sequence 41, Appl	27,	Sequence 41, Appl Sequence 47, Appl	Sequence 2, Appli Sequence 2, Appli	Sequence 6, Appli	, ,	Sequence 12, Appl	Sequence 13, Appl	Sequence 2, Appli
US-08-190-802A-173 US-08-477-346-70	US-08-4//-346-129 US-08-477-346-173 US-08-190-8028-27	US-08-190-802A-41 US-08-190-802A-41 US-08-190-802A-47	US-08-477-346-27	US-08-477-346-41 US-08-477-346-47	US-09-550-338-2 US-08-366-490-2	US-08-366-490-6	US-08-860-483A-6	US-08-860-483A-12	US-08-860-483A-13	US-08-679-405-2
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31	31	317	317	317	523 592	592	592	596	296	009
34.6	34.6	34.6	34.6	34.6 34.6	34.6 34.6	34.6	34.6	34.6	34.6	34.6
37	37	37	37	37	37	37	37	37	37	37
8 6 6	31 32	1 8 6 4 8 4	35	35 37	8 6 8 8	40	42	43	44	45

ALIGNMENTS

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US-08-93-326-18

is Sequence 18, Application US/08953326

is Sequence 18, Application US/08953326

is General INFORMATION:

is APPLICANT: Barbet, Anthony F.

APPLICANT: Ganta, Roman R.

is APPLICANT: Buridge, Michael J.

APPLICANT: Rurangirwa, Fred R.

APPLICANT: Rurangirwa, Fred R.

APPLICANT: Wandan Nawan M.

TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of TITLE OF INVENTION: Animals and Humans

FILE REFERENCE: UF-167C1

CURRENT APPLICATION NUMBER: US/08/953,326

CURRENT FILING DATE: 1997-10-17

EARLIER APPLICATION NUMBER: 08/953,326

EARLIER FILING DATE: 1997-10-17

EARLIER FILING DATE: 1997-10-17

EARLIER FILING DATE: 1997-10-17

EARLIER FILING DATE: 1996-10-17

WUMBER OF SEQ ID NOS: 24

COMMANDER: OF SEQ ID NOS: 24
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100.0%; Pred. No. 4.9e-10;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-733-230-4
; Sequence 4, Application US/08733230
; Patent No. 6025338
; GENERAL INFORMATION:
; APPLICANT: Barbet, Anthony F.
; APPLICANT: Ganta, Roman Reddy
; APPLICANT: McGuire, Travis C.
; APPLICANT: Burridge, Michael J.
; APPLICANT: Nyika, Aceme
; APPLICANT: Rurangirwa, Fred R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CORGANISM: Ehrlichia chaffeensis
US-08-953-326-18
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Best Local Similarity
Matches 20; Conserv
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Sequence 4, Application US/08953326

Patent No. 6251872

GENERAL INFORMATION:
APPLICANT: Genta, Anthony F.
APPLICANT: McCulre, Travis C.
APPLICANT: McCulre, Travis C.
APPLICANT: Buridge, Michael J.
APPLICANT: Multa, Acceme
APPLICANT: Multa, Acceme
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
TITLE OF INVENTION: Animals and Humans
TITLE OF INVENTION: Animals and Humans
FILE REFERENCE: UF-1670.
CURRENT APPLICATION NUMBER: US/08/953,326

CURRENT FILING DATE: 1997-10-17

EARLIER RELIGATION NUMBER: 08/733,230

EARLIER PLING DATE: 1997-10-17

SEALLIER PLING DATE: 1997-10-17

NUMBER OF SEQ ID NOS: 24

SEGULDANCE: PatentIN Ver: 2.0
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APPLICANT: Mahan, Suman M.

TITLE OF INVENTION: Nucleic Acid Vaccines Against
TITLE OF INVENTION: Rickettsial Diseases and Methods of Use
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STRATE: FL
STRATE: FL
STRATE: FL
STRATE: Floppy disk
COUNTY: USA
ZIP: FLOPPY disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PREMENTIN RC-DOS/MS-DOS
SOFTWARE: PARENTIN RC-DOS/MS-DOS
SOFTWARE: PLOMATA:
PRELIZATION NUMBER: US/08/733,230
FILING DATE:
CLASSIFICATION: S14
ATTORNEY-AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTATION NUMBER: 65,965
REFERENCE/DOCKET INFORMATION:
TELEFRAX: 352-372-8800
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
LEMSTH: 280 amino acids
TPDE: MINER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 107; DB 3; Length 280; Best Local Similarity 100.0%; Pred. No. 5e-10; Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NTTVGVFGLKQNWDGSAISN 20
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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RESULT 4

1. Sequence 17

1. Sequence 17

1. Sequence 17

2. Sequence 17

3. Sequence 17

4. Sequence 17

5. Sequence 17

6. Application Us/08953326

7. APPLICANT: Barbet, Anthony F.

APPLICANT: Ganta, Roman R.

APPLICANT: Mariage, Michael J.

APPLICANT: Wirka, Accoman R.

APPLICANT: Wirka, Accoman R.

APPLICANT: Wahan, Suman M.

7. TITLE OF INVENTION: Naniels and Humans

7. TITLE OF INVENTION: Animals and Humans

7. TITLE OF INVENTION: Animals and Humans

7. TITLE OF INVENTION: Animals and Humans

7. TITLE OF INVENTION: MUMBER: US/08/953,326

6. URRENT FILING DATE: 1997-10-17

6. SEALIER FILING DATE: 1997-10-17

7. SEALIER FILING DATE: 1996-10-17

8. SEQ ID NO 17

LENGTH: 280

7. TYPE: PRT

8. ORGANISM: Bhrlichia chaffeensis

15. US-08-953-326-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            us-vu-vs3-s4b-12
; Sequence 15, Application US/08953326
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Barbet, Anthony F.
APPLICANT: Ganta, Roman R.
APPLICANT: Ganta, Roman R.
APPLICANT: Murridge, Michael J.
APPLICANT: Murridge, Michael J.
APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: UNCleic Acid Vaccines Against Rickettsial Diseases of TITLE OF INVENTION: Anthals and Humans
FILE REFRENCE: UF-167C1
CURRENT FILING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1996-10-17
EARLIER FILING DATE: 1996-10-17
SEARLIER FILING DATE: 1996-10-17
SEARLIER FILING DATE: 1996-10-17
SUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
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Query Match
100.0%; Score 107; DB 4; Length 280;
Best Local Similarity 100.0%; Pred. No. 5e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 280;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 91; DB 4; Pred. No. 2.1e-07; 2; Mismatches 1.
                                                                                                          1 NTTVGVFGLKQNWDGSAISN 20
                                                                                                                                            60 NTTVGVFGLKQNWDGSAISN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 85.0%;
Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 NTTIGVFGLKQDWDGSTIS 78
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Barbet, Anthony F.
APPLICANT: Barbet, Roman Reddy
APPLICANT: Ganta, Roman Reddy
APPLICANT: McGuire, Travis C.
APPLICANT: Burridge, Michael J.
APPLICANT: Nyika, Aceme
APPLICANT: Rurangirwa, Fred R.
APPLICANT: Rurangirwa, Fred R.
APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Nucleic Acid Vaccines Against
TITLE OF INVENTION: Rickettsial Diseases and Methods of Use
                                                                                                                                                                                                                                                                                    Score 60; DB 4; Length 278;
Pred. No. 0.025;
6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 51; DB 3; Length 287; Pred. No. 0.77; 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA

ZIP: 33606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,230
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
  EARLIER FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/733,230
EARLIER FILING DATE: 1996-10-17
NUMBER OF SEQ ID NOS: 24
SEQ TRANSE: PATENTIN Ver. 2.0
SEQ ID NO 16
LENGTH: 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08733230 Patent No. 6025338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
ATORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF-1
TELECOMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEPHONE: 352-375-800
                                                                                                                                                                   TYPE: PRT
ORGANISM: Ehrlichia chaffeensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36,965
                                                                                                                                                                                                                                                                                         56.1%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                   1 NTTVGVFGLKQNWDGSAISN 20
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Best Local Similarity 69.2%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 287 amino acids
amino acid
                                                                                                                                                                                                                                                                                         Ouery Match 56.1
Best Local Similarity 50.0
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 352-372-5800 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear;
; MOLECULE TYPE: protein
US-08-733-230-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 TVGVFGLKQNWDG 15
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                                                                                                                                                                                                                       US-08-953-326-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: G
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20, Application US/08953326

Patent No. 621872

GENERAL INFORMATION:

APPLICANT: Barbet, Anthony F.

APPLICANT: Buridge, Michael J.

APPLICANT: Buridge, Michael J.

APPLICANT: Rurangirwa, Fred R.

APPLICANT: Rurangirwa, Fred R.

APPLICANT: Rurangirwa, Fred R.

APPLICANT: Najka, Aceme

APPLICANT: Najka, Aceme

TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of

TITLE OF INVENTION: Number: US/08/953,326

CURRENT APPLICATION NUMBER: US/08/953,326

CURRENT APPLICATION NUMBER: US/08/953,326

CURRENT APPLICATION NUMBER: 08/953,326

CURRENT RILING DATE: 1997-10-17

EARLIER FILING DATE: 1997-10-17

EARLIER PLING DATE: 1997-10-17

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 20

LENGTH: 133
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APPLICANT: Ganta, Roman R.
APPLICANT: Ganta, Roman R.
APPLICANT: Ganta, Tavis C.
APPLICANT: Burridge, Michael J.
APPLICANT: Burridge, Michael J.
APPLICANT: Rurangirwa, Fred R.
APPLICANT: Rurangirwa, Fred R.
APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of TITLE OF INVENTION: Animals and Humans
FILE REFERENCE: UF-167C1
                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                   68.2%; Score 73; DB 4; Length 286; 68.4%; Pred. No. 0.00019; Live 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 61.5; DB 4;
Pred. No. 0.006;
3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/08/953,326
CURRENT FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/953,326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16, Application US/08953326
Patent No. 6251872
; SEQ ID NO 15
; LENGTH: 286
; TYPE: PRT
: ORGANISM: Ehrlichia chaffeensis
US-08-953-326-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.48;
                                                                                                                                                                                                                                                              1 NTTVGVFGLKQNWDGSAIS 19
                                                                                                                                                                                                                                                                                             60 NTTVGVFGIEQDWDRCVIS 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||| |:|||:|| | |||:
62 TTV-VYGLKENWAGDAISS 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 57.5
Best Local Similarity 68.4
Matches 13; Conservative
                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT; ORGANISM: Ehrlichia canis
US-08-953-326-20
                                                                                                                                                                   Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    US-08-953-326-20
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                                                                                                                                                                                                 APPLICANT: Barbet, Anthony F.
APPLICANT: Ganta, Roman R.
APPLICANT: Ganta, Roman R.
APPLICANT: Ganta, Roman R.
APPLICANT: Ganta, Roman R.
APPLICANT: Burridge, Michael J.
APPLICANT: Burridge, Michael J.
APPLICANT: Burridge, Michael J.
APPLICANT: Mahan, Suman M.
APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of TITLE OF INVENTION: Animals and Humans
APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Animals and Humans
APPLICANT: MAHAN Suman M.
TITLE OF INVENTION: NUMBER: US/08/953,326
CURRENT FILING DATE: 1997-10-17
SARLIER APPLICATION NUMBER: 08/733,230
SARLIER PILING DATE: 1996-10-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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US-08-840-146-19
Sequence 19, Application US/08840146
Petent No. 6037173
Petent No. 6037173
Petent No. 6037173
Petent No. 6037170:
APPLICANT Glucksmann, M. Alexandra
APLICANT Glucksmann, M. Alexandra
TITLE OF INVENTION: DIAGNOSTIC COMPOSITIONS AND METHODS AND
TITLE OF INVENTION: DIAGNOSTIC ASSAYS FOR DISEASES INVOLVING TRBP
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
CITY: MA
COUNTRY: USA
ZIP: 02109-2170
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Pred. No. 0.77;
2; Mismatches 2; Indels
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MEDIUM TYPE: FLOPPY disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pattentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 11-APR-1997
CLASSIFICATION: 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-APR-1997
                                                                                                          US-08-953-326-2
Sequence 2. Application US/08953326
Patent No. 6251872
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MIR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Cowdria ruminantium
US-08-953-326-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 47.7%;
Best Local Similarity 69.2%;
Matches 9; Conservative
3 TVGVFGLKQNWDG 15
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                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19. Application US/09360220
Fatent No. 6046308
GENERAL INFORMATION:
APPLICANT: Glucksmann, M. Alexandra
TITLE OF INVENTION: THERAPETITIC COMPOSITIONS AND METHODS AND
TITLE OF INVENTION: DIAGNOSTIC ASSAYS FOR DISEASES INVOLVING TRBP
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                         Query Match
38.3%; Score 41; DB 3; Length 365;
Best Local Similarity 60.0%; Pred. No. 44;
Matches 6; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 365;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: MA
COUNTRY: USA
ZIP: R2109-2170
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
COMPUTER: PLOPS MISK
COMPUTER: PLOPS MISK
COMPUTER: PLOPS MISK
COMPUTER: PACATION DATA:
APPLICATION NUMBER: US/09/360,220
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/840,146
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: ALOLG/ Beth E.
REGISTRATION NUMBER: MIA-018.01
TELEDAMINICATION INDER: MIA-018.01
TELECOMMUNICATION INDER: MIA-018.01
TELECOMMUNICATION INDER: MIA-018.01
TELECOMMUNICATION INDER: MIA-018.01
TELEFRAX: 617-832-1000
TANDOMMET OF DESCRIPTION OF THE MIA-DAMMET MIA-018.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.3%; Score 41; DB 3; 60.0%; Pred. No. 44; tive 3; Mismatches
                                            19:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 19
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ. ID NO: 19
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity ov...
6, Conservative
                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-840-146-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-360-220-19
                                                                                                                                                                                                                                                                                                                                                                        334 KNWDGSPVSS 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 QNWDGSAISN 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 QNWDGSAISN 20
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US-09-360-220-19
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Gaps
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Batent No. 5865787

GENERAL INFORMATION:

APPLICANT: Sincerman, Robert H.

APPLICANT: SenGupta, Dibyendu N.

TITLE OF INVENTION: Fransgenic Plants Co-Expressing A
TITLE OF INVENTION: Functional Human 2-5A System

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Holland & Knight

STREET: One E. Broward Boulevard, #1300

CITY: Fort Lauderdale

STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 400;
                                                                                                       OPERATING SYSTEM: PC^DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 2;
Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTICATION NOMBER 1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: CL11363-16(C)
TELECOMMUNICATION INFORMATION:
TELECHOMORE: 305/468-7811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41;
                                                                                                                                                                                                                                                                                                                                      NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: CL11363-16
TELECAMUNICATION IRPORMATION:
TELEPHONE: 305/527/2498
TELEFAX: 305/764/4996
                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/198,973
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/487,797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
              ZIP: 33301
COMPUTER READABLE FORM:
MEDUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 305/764/4996
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.3%;
60.0%;
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Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US
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COUNTRY:
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                                                   Sequence 11, Application US/08436771
Patent No. 5861300
GENERAL INFORMATION:
APPLICANT: SanGupta, Dibyendu N.
TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,
TITLE OF INVENTION: Cells and Methods
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & MadDRESSEE: Russell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.3%; Score 41; DB 2; Length 400; 60.0%; Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/08434998
Patent No. 5866781
GENERAL INFORMATION:
APPLICANT: Sluverman, Robert H.
APPLICANT: SenGupta, Dibyendu N.
TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors, TITLE OF INVENTION: Cells and Methods
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: CL11363-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/198,973
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                         STREET: 200 E. Broward Boulevard CITY: Fort Lauderdale STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/436,771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 200 E. Broward Boulevard CITY: Fort Lauderdale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 305/527/2498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 400 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
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333 KNWDGSPVSS 342
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                US-08-436-771-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-436-771-11
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PCT-U595-02058
PCT-U595-02058
PCT-U595-02058
SEQUENCE 11, Application PC/TUS9502058
GENERAL INFORMATION:
TITLE OF INVENTION: Antivital Transgenic Plants, Vectors, TITLE OF INVENTION: Cells and Methods
ITLE OF INVENTION: Cells and Methods
TITLE OF INVENTION: Cells and Methods
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rusden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Rusden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Rusden, Barnett, McClosky, Smith, Schuster & COUNTRY: USA
INTERFERENCE RESPONDENCE ADDRESS:
COUNTRY: USA
INTERFERENCE PETUL Lauderdale
STATE: Florida
COUNTRY: USA
INTERFERENCE PETUL FORM:
MCDION TYPE: Florida
COUNTRY: USA
INTERFERENCE PETUL FORM:
MCDION TYPE: Florida
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: PCT/US95/02058
FILING DATE: 18-FEB-1994
SPLICATION NUMBER: USA
FILING DATE: 18-FEB-1994
SPLICATION NUMBER: USA
STATONRY-AGENT INPORMATION:
NAME: MARION PETERISTICS:
TELEROMATION NUMBER: CL11363-16
FELENGTH: 400 amino acids
STRANDENESS: SINGLE
STRANDENESSES INGLE
STRANDENESS: SINGLE
STRANDENESS: SINGLE
STRANDENESS: SIN
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TELEFAX: 305/463-2030
; INFORMATION FOR SED ID NO: 11:
SEGUENCE CHARACTERISTICS:
TYPE: amino acid
TYPE: amino acid
STRANDENNESS: sindle
TOPOLOGY: linear
US-08-487-797-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :||||| :|:
333 KNWDGSPVSS 342
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Search completed: March 14, 2002, 09:07:40 Job time: 841 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

March 14, 2002, 09:07:41; Search time 54.54 Seconds (without alignments) 7.427 Million cell updates/sec Run on:

US-09-765-739A-6 97

Perfect score: Sequence:

1 NPTVALYGLKQDWEGISS 18

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

212252 segs, 22503292 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:* Issued_Patents_AA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
TITLE OF INVENTION: Animals and Humans
TITLE OF INVENTION: Animals and Humans
FILE REPERENCE: UF-16721
CURRENT FILING DATE: 1997-10-17
EARLIER PPLICATION NUMBER: 08/953,326
EARLIER PILING DATE: 1997-10-17
EARLIER PILING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-17
NUMBER OF SEQ ID NOS: 24
SOUTHWARE: PATENTIN VET: 2.0

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Result		Query				
No.	Score	Match	Length	60	QI	Description
Ħ	26	100.0	278	4	US-08-953-326-16	Sequence 16, Appl
7	62	63.9	280	4	-953-326	17,
m	58	9.	276	4	US-08-953-326-18	18,
4	58	59.8	280	٣	-733-2	4, 7
5	58	6	280	7	-08-953	4
ø	52	ω.	287	٣	-733-	7
7	52	53.6	287	4	-08-953	7
80	51	•	286	4	US-08-953-326-15	15,
6	48	49.5	133	4	3-953	20,
10	42	43.3	915	4	9-346	2, 7
11	42	43.3	928	٦	3-474	11,
12	42	43.3	928	7	47	11,
13	42	43.3	928	П	3-472-29	11,
14	42	43.3	928	٦	മ	11,
15	42	43.3	928	~	US-08-478-341-11	11,
16	4	43.3	928	က	US-08-996-733-11	11,
17	39.5	40.7	66	~	US-08-860-577-3	3, A
18	39	40.2	263	П		7,
1.9	39		263	7	US-07-988-430-7	7,
20	39	•	263	Н		7,
21	39		263	-	US-08-488-113B-7	7,
22	39	40.2	263	Н	-08-47	7,
23	38		263	7	-64	7,
24	39	•	263	4	US-08-839-765-7	7
25	39	40.2	263	4	US-09-136-389-7	7,
56	39	•	263	Ŋ	2-09487	Sequence 7, Appli
27	39	40.2	609	~	US-07-798-776-2	7

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Gaps

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Query Match 100.0%; Score 97; DB 4; Length 278; Best Local Similarity 100.0%; Pred. No. 3.6e-09; Matches 18; Conservative 0; Mismatches 0; Indels

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ORGANISM: Ehrlichia chaffeensis US-08-953-326-16

LENGTH: 278 TYPE: PRT SEQ ID NO 16

Sequence 17, Application US/08953326
Patent No. 6251872
GENERAL INFORMATION:
APPLICANT: Barbet, Anthony F.
APPLICANT: Ganta, Roman R.
APPLICANT: Burridge, Michael J.
APPLICANT: WIXIA, Aceme
APPLICANT: NYIKA, Aceme
APPLICANT: Rurangirwa, Fred R.

US-08-953-326-17

8 6 6	3,9	440	000	m m n	US-08-251-288A-2 US-09-298-819A-2	
30 37 37	38 38 38 38	თ თ თ ო ო ო	68 73 86	w 4 4	US-08-947-965-2 US-08-989-385-1 US-09-346-237-1	Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli
3 3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	37.5	60000	147 36 39	Б	US-08-840-062-4 PCT-US93-11703-24 US-08-499-568-15	4, 24, 15,
36 337 39	37.8	88888	3 8 8 9 6 9 6 9 6 9 6 9 6 9 6 9 9 9 9 9 9	004°	US-08-793-958-15 US-08-956-998-2 US-08-740-223A-18 US-08-947-965-76	1217
044 442 33	37 37 37 37		.1 553 .1 575 .1 595 .1 820	4 2 11 1	1 US-07-683-9578-3 1 US-07-683-9578-3 2 US-08-677-049-11 4 US-09-313-677-21	2, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3,
	3,37	& & K K	Q Q Q E	4 4	US-09-313-677-2 US-09-313-677-19 ALIGNMENTS	Sequence 2, Appli Sequence 19, Appl
RESULT 1 US-08-953-326-16 ; Sequence 16, Applic. Patent No. 6251872 ; GENERAL INFORMATION	1 3-326- 5e 16, No. 6	16 Appli 251872 RMATIO	SULT 1 -08-953-326-16 Sequence 16, Application US/08953326 Patent No. 625.872 GENERAL INFORMATION:	80/:	953326	
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT:	CANT	Barbet, Ganta, McGuire Burridg Nyika, Rurangi	Barbet, Anthony F Ganta, Roman R. GacGuire, Travis C Burridge, Michael Nyika, Aceme Nyika, Aceme	C. C.	*3	

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US-08-953-326-18
Factor IN 0. 6251872
Fatent No. 6251872
FAPLICANT: Barbet, Anthony F.
APPLICANT: Ganta, Roman R.
APPLICANT: Ganta, Roman R.
APPLICANT: Wikka, Aceme
APPLICANT: Wikka, Aceme
TAPLICANT: Wikka, Aceme
FAPLICANT: Wikka, Aceme
APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Animals and Humans
FILE REFERENCE: UF-16721
CURRENT PAPLICATION NUMBER: 08/0953,326
CURRENT PAPLICATION NUMBER: 08/0953,326
CURRENT FILING DATE: 1997-10-17
FEARLIER APPLICATION NUMBER: 08/793,326
SCHEMARE: PALCATION NUMBER: 08/733,230
SCHEMARE: PALCATION NUMBER: 1996-10-17
SCHEMARE: PALCATION NUMBER: 208/733,230
SCHEMARE: PACHICATION NUMBER: 208/733,230
SCHEMARE: PACHICATION NUMBER: 208/733,230
SCHEMARE: PACHICATION NUMBER: 208/733,230
SCHEMARE: PACHICATION NUMBER: PACHICA
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APPLICANT: Mahan, Suman M.

TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of TITLE OF INVENTION: Nucleic and Humans
FILE REFERENCE: UF-16701
CURRENT APPLICATION NUMBER: 08/0953,326
CURRENT FILING DATE: 1997-10-17
EARLIER PELIGNON NUMBER: 08/953,326
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-17
STRING DATE: 1996-10-17
STRING DATE: 1996-10-17
STRING DATE: 1996-10-17
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Pred. No. 0.0042;
4; Mismatches 2; Indels
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APPLICANT: Barbet, Anthony F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Ehrlichia chaffeensis
US-08-953-326-17
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US-08-953-326-18
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60.0%;
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Best Local Similarity 60.0
Matches 9; Conservative
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Matches 9; Conservative
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59 NTTVGVFGLKQNWDG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
US-08-733-230-4
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PAPLICANY: Gantle, Reman Reddy
APPLICANY: Gantle, Travis C.
APPLICANY: BUILDING, Michael J.
APPLICANY: BUILDING, Saman M.
APPLICANY: BUILDING, Saman M.
APPLICANY: BUILDING, Saman M.
APPLICANY: BUILDING, Saman M.
APPLICANY: BUILDING, MICHAEL A.
APPLICANY: BUILDING, BUILDING, A.
APPLICANY: BUILDING, APPLICANY: BUILDING
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RESULT 8

US-08-953-326-15

Sequence 15 Application US/08953326

Sequence 15 Application US/08953326

Sequence 15 Application US/08953326

Sequence 15 Application US/08953326

Setcor No. 6251872

APPLICANT: Barbet, Anthony F.

APPLICANT: Ganta, Roman R.

APPLICANT: Buridge, Michael J.

APPLICANT: Wahan, Suman R.

APPLICANT: Wahan, Suman M.

TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of TITLE OF INVENTION: Animals and Humans

FILE REFERENCE: UF-16701

CURRENT APPLICATION NUMBER: US/08/953,326

CURRENT FILING DATE: 1997-10-17

EARLIER APPLICATION NUMBER: 08/953,326

EARLIER FILING DATE: 1997-10-17

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PatentIN Ver. 2.0

SEROIT NO 15
                                                       GENERAL INFORMATION:
APPLICANT: Barbet, Anthony F.
APPLICANT: Barbet, Anthony F.
APPLICANT: Barbet, Anthony F.
APPLICANT: Ganta, Roman R.
APPLICANT: Burridge, Michael J.
APPLICANT: Burridge, Michael J.
APPLICANT: Wahan, Suman M.
TITLE OF INVENTION: Animals and Humans
TITLE OF INVENTION: Animals and Humans
TITLE OF INVENTION: Animals and Humans
FILE REFERENCE: UF-16701
CURRENT APPLICATION NUMBER: US/08/953,326
EARLIER APPLICATION NUMBER: 08/953,326
EARLIER PILING DATE: 1997-10-17
EARLIER PILING DATE: 1997-10-17
EARLIER PILING DATE: 1997-10-17
SERRIER PILING DATE: 1996-10-17
NUMBER OF SEQ ID NOS: 24
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 51; DB 4; Length 286;
Pred. No. 0.35;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 52;
Pred. No.
                      Sequence 2, Application US/08953326 Patent No. 6251872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Ehrlichia chaffeensis
US-08-953-326-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Cowdria ruminantium
US-08-953-326-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.6%;
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50.0%;
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Best Local Similarity 50.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 43.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 TVALYGLKQDWEGISS 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ::|||:||:|:
63 TQTVFGLKKDWDGVKT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
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0
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APPLICANT: MCGULK, Travis C.
APPLICANT: Muritage, Michael J.
APPLICANT: Nurian Nika, Aceme
APPLICANT: Rurangirwa, Fred R.
APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Nucleic Acid Vaccines Against
TITLE OF INVENTION: Rickettsial Diseases and Methods of Use CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 52; DB 3; Length 287;
Pred. No. 0.24;
                                                                                                                                               Score 58; DB 4; Length 280;
Pred. No. 0.021;
                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O8/733,230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: Saliwanchik & Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08733230
Patent No. 6025338
GENERAL INFORMATION:
APPLICANT: Barbet, Anthony F.
APPLICANT: Ganta, Roman Reddy
                                     TYPE: PRT

CRGANISM: Ehrlichia chaffeensis

US-08-953-326-4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: UF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
                                                                                                                                               59.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 287 amino acids TYPE: amino acid
                                                                                                                                                                   Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   352-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | ::|||:||:|: : | 63 TQTVFGLKKDWDGVKT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 TVALYGLKQDWEGISS 18
                                                                                                                                                                                                                                   1 NPTVALYGLKODWEG 15
                                                                                                                                                                                                                                                           | || ::||||:|
60 NTTVGVFGLKQNWDG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-733-230-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
STREET: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
SEQ ID NO 4
LENGTH: 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                            US-08-733-230-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: C
STATE:
                                                                                                                                                 Query Match
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RESULT

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NESULT 140-11
Sequence 11, Application US/08474140
Sequence 11, Application Sequence 11, TILE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K Street, N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/08477630
Patent No. 5721120
GENERAL INFORMATION:
GENERAL INFORMATION:
HILLPE
APPLICANT: DEBERER, PHILIPE
TITLE OF INVENTION: PULULULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PULULANASE AND THE USES THEREOF
TITLE OF INVENTION: PULULANASE AND THE USES THEREOF
TITLE OF INVENTION: PULULANASE AND THE USES THEREOF
WUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42; DB 1; Length 928;
Pred. No. 52;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
MEDIUW TYPE: Floppy disk
COMPUTER: EN PC Compatible
COMPUTER: EN PC COMPATIBLE
COMPUTER: EN PC COMPATIBLE
COMPUTER: DAP COMPATIBLE
COMPUTER: DAP COMPATIBLE
CORREST APPLICATION NUMBER: US/08/474,140
FILING DATE: 07-JUN 1995
CLASSIFICATION NUMBER: US/08/474,140
FILING DATE: 07-JUN 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Willham F Gadiano, Esq.
REFERENCE/COCKET UNBER: 37,136
REFERENCE/COCKET UNBER: 4121-41
TELEPHONE: (202) 429-0625
TELEFAX: (202) 23-150
TELEFAX: (503) 33-150
INFORMATION FOR EXQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 928 mmino acids
TWENTH: 928 mmino acids
        Mismatches
     3;
                                                                                         628 NPGIALYG--EPWTGGTS 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   641 NPGIALYG--EPWTGGTS 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acids
TOPOLOGY: lin-
                                                        1 NPTVALYGLKQDWEGISS 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NPTVALYGLKQDWEGISS 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 43.3
Best Local Similarity 50.0
Matches 9; Conservative
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-474-140-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
US-08-477-630-11
     9;
     Matches
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                                                                                                                                                                                                                      APPLICANT: Barbet, Anthony F.
APPLICANT: Garbet, Anthony F.
APPLICANT: Garbet, Anthony F.
APPLICANT: Garbet, Travis C.
APPLICANT: Burridge, Michael J.
APPLICANT: Burridge, Michael J.
APPLICANT: Wilka, Acceme
APPLICANT: Whita, Acceme
TITLE OF INVENTION: Wucleic Acid Vaccines Against Rickettsial Diseases of
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
TITLE OF INVENTION: Mulmans and Humans
TITLE OF INVENTION: Mulmars: US/08/953,326
TITLE APPLICATION NUMBER: US/08/953,326
CURRENT FILING DATE: 1997-10-17
CURRENT FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/733,230
EARLIER PILING DATE: 1996-10-17
SCRTURE PILING DATE: 1996-10-17
SCRTURE PILING DATE: 1996-10-17
SCRTURE PILING DATE: 1996-10-17
SEQ ID NOS: 24
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09346237A
Sequence 2, Application US/09346237A
Fatent No. 6265197
GENERAL INFORMATION:
APPLICAMY: Bisgard'Frantzen, Henrik
APPLICAMY: Stendsen, Allan
TITLE OF INVENTION: Starch Debranching Enzymes
FILE REFERENCE: 5629.200.US
CURRENT APPLICATION UNBER: US/09/346,237A
CURRENT PILING DATE: 1999-07-01
EARLIER APPLICATION NUBBER: PA 1998 00868
EARLIER PILING DATE: 1998-07-02
EARLIER FILING DATE: 1998-07-02
SEARLIER FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 48; DB 4
Pred. No. 0.46;
3; Mismatches
                                                                                                                                                  Sequence 20, Application US/08953326
Patent No. 6251872
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Bacillus deramificans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: PEPTIDE
; LOCATION: (1)...(915)
; OTHER INFORMATION: Pullulanase
US-09-346-237-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.3%;
50.0%;
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| :||||::| | |||
62 TTVVYGLKENWAGDAISS 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 55.69
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Ehrlichia canis
US-08-953-326-20
| | | ::|::||:
60 NTTVGVFGIEODWD 73
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Best Local Similarity
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Sequence 11, Application US/08474545
Pattent No. 5736375
GENERAL INFORMATION:
APPLICANT: DEWEER, PHILIPPE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
CORRESPONDENCE: 15
CORRESPONDENCE: MILLIAN BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K Street, N.W., Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 928; 52;
                                                                                                                                                                                                                            Length 928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                            Score 42; DB 1
Pred. No. 52;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.3%; Score 42; DB 50.0%; Pred. No. 52; Live 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , v
.......: US/08/474,545
07-JUN-1995
NN: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 4121-43
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/474
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, Esq
REGISTRATION NUMBER: 37,136
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                              43.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                 641 NPGIALYG--EPWTGGTS 656
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                                                                                    LENGTH: 928 amino acids
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Best Local Similarity 50.0
Matches 9; Conservative
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Best Local Similarity 50.0
Matches 9; Conservative
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                                                                                                                                             ; MOLECULE TYPE: protein US-08-472-293-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                     TYPE: amino acids
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                    qq
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APPLICANT: DEREER, PHILIPPE
APPLICANT: DEREER, PHILIPPE
APPLICANT: DEREER, PHILIPPE
APPLICANT: ADMORY, ANYOINE
TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
NUMBER OF INVENTION: PULLULANASE AND THE USES THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K Street, N.W., Suite 200
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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ZIP: 20006
COMPUTER READBLE FORM:
MEDLINM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BATCHIN FC-DOS/MS-DOS
SOFTWARE: PatcHIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,293
FTLING DATE: 07-JUN-1995
FTLING DATE: 07-JUN-1995
                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/477,630
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB 1;
Pred. No. 52;
3; Mismatches
  2000 K Street, N.W., Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-44
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
                                                                                                                                                                                                                                                                                                                                                  4121-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/08472293 Patent No. 5731174
                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Willem F. Gadiano, ESG.
REGISTRATION UNDRER: 37,136
REFERENCE/DOCKET UNDRER: 4121-
TELECOMMUNICATION INFORMATION:
TELEFRAX: (202) 429-0625
TELEFRAX: (202) 29-1850
TELEFRAX: 650 383-5605
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 928 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43.3%;
50.0%;
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Best Local Similarity 50.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-630-11
    LITY: Washington STATE: D C
                                                             U.S.A.
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US-08-472-293-11
                                                             COUNTRY:
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1;

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Query Match
43.3%; Score 42; DB 2; Length 928;
Best Local Similarity 50.0%; Pred. No. 52;
Matches 9; Conservative 3; Mismatches 4; Indels
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Search completed: March 14, 2002, 09:07:42 Job time: 843 sec

pp δλ

1;

Gaps 2, -

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/SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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/SIDSB/gcgdata/geneseq/geneseqp/AA1986.DAT:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                       522463 seqs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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97
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                                                                                                                                                                                                                                                                                     Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /SIDSB/gcgdata/geneseq/geneseqp/An1999.DAT:
/SIDSB/gcgdata/geneseq/geneseqp/An1990.DAT:
/SIDSB/gcgdata/geneseq/geneseqp/An1990.DAT:
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/SIDSB/gcgdata/geneseq/geneseqp/An1999.DAT:
/SIDSB/gcgdata/geneseq/geneseqp/An1999.DAT: /SIDS8/gcgdata/geneseg/genesegp/AA2001.DAT:*

E. chafeensis OMP-Ehrlichia chaffeen Ehrlichia chaffeen Variable surface a E. chafeensis OMP-E. canis P30 prote E. chafeensis p28 Ehrlichia chaffeen E. chafeensis OMP-Ehrlichia chaffeen Variable surface a Description SUMMARIES AAU04198 AAY06948 AAY06959 AAY06942 AAW51093 AAY06947 AAB36187 AAY 06945 AAW51094 AAB36188 AAU04197 П 19 22 22 22 23 20 20 20 20 20 20 Query Match Length DB 2280 100.0 100.0 100.0 100.0 90.7 63.9 63.9 63.9 60.8 Score 4 5 7 7 10 11 11 Result Š

WPI; 1998-251232/22. N-PSDB; AAV07179.

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12	28	٠. م	276	5	AAW51095	
T 3	28	٠.	7.76	7.7	AAB36189	a chaitee
14	28	δ.	276	22	AAU04199	S.
15	28	δ.	280	19	AAW51089	
16	28	ص	280	21	AAB36183	
17	58	6	280	22	AAU04193	ajor antigenic p
18	28	δ.	281	20	AAY06943	. chafeensis O
19	26	7	280	20	AAY06962	Р30-2 р
20	26	7	280	21	AAY71479	canis
21	53	4	278	21	AAY71477	hrlichia canis
22	53	4.	307	20	AAY06961	E. canis P30-1 pro
23	52	ω.	287	19	AAW51088	ruminan
24	52	Э.	287	21	AAB36182	
25	52	ω,	287	22	AAU04192	Major antigenic pr
56	51	٠	286	13	AAW51092	Ehrlichia chaffeen
27	51	2	286	20	AAY06946	E. chafeensis OMP-
28	51	ς.	286	21	AAB36186	æ
. 29	51	2	286	22	AAU04196	
30	48	6	132	22	AAU04201	surface
31	48	6	133	19	AAW51097	
32	48	6	133	21	AAB36191	canis
33	48	ο.	133	21	AAY71480	a canis
34	48	φ.	276	20	AAY06964	P30-4
35	48	φ.	283	21	AAY71478	canis
36	47	48.5	904	20	AAY21976	
37	43		20	21	AAB33357	
38	43	44.3	23	21	AAB33358	radiata
39	43		237	21	AAB33257	Pinus radiata tran
40	42		187	21	AAY81775 .	O
41	42		815	22	AAE05695	
42	42		817	22	AAE05694	deramifi
43	42	•	826	20	AAY31748	ຜ
44	42		830	20	AAY31747	Bacillus deramific
45	42	•	⊣	21		Pullulanase amino
					ALIGNMENTS	
RESULT	-					
AAW51093	1					
	AAW51093 sta	standard;	Protein;		278 AA.	
AC AAW:	AAW51093;					
14	-SEP-1998	(firs	(first entry	ζ.		
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DE Ehr.	Ehrlichia c	chaffeensis VSA3	sis vs		protein.	

MAP1 homologue; variable surface antigen; VSA3; rickettsia; McGuire TC; "putative signal peptide" Mahan SM, Ganta RR, Location/Qualifiers 96US-0733230 97WO-US1904 Barbet AF, Burridge MJ, Nyika A, Rurangirwa FR; 'note≅ Ehrlichia chaffeensis. (UYFL) UNIV FLORIDA WO9816554-A1. 17-OCT-1997; 17-0CT-1996; 23-APR-1998 DNA vaccine Peptide__ ~

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The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafensis and E. canis. The E. chafensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to 2) shown in AAY06943-958. The E. canis proteins form part of the P30 family and
                                                                                                    This is the full-length variable surface antigen VSA3 protein of Bhrlichia chaffeensis. Its amino acid sequence was deduced from a partial open reading frame (ORF5) of a genomic locus (see AAV07179) of E. chaffeensis that was obtained on the basis of homology to the major antigenic protein MAPI (see AAM51088) of Cowdria runninantium. This genomic locus included 5 ORFs encoding similar, but non-identical proteins (see AAM51091-95). A claimed composition comprises a nucleic acid (see AAV107176-82) encoding a polypeptide (see AAM51088-99) that elicits a protective immune response against ricketrial pathogen. The nucleic acid is used, in human or veterinary medicine, in vaccines to protect against Rickettsia, but and Cowdria species. The Ehrlichia antigenic polypeptides can be used diagnostically to detect antibodies associated with Ehrlichia infection (claimed).
             Composition containing nucleic acid encoding rickettsial antigen - useful for, e.g. stimulating protective immune response in humans or
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30; detection; dog.
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                                                                                                                                                                                                                                                                                                                                                                                                 Length 278;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                 Score 97; DB 19;
Pred. No. 2.2e-08;
; Mismatches 0;
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                                                                          Claim 3; Fig 2A-B; 39pp; English.
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Best Local Similarity 100.0%;
Matches 18; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohashi N, Rikihisa Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ehrlichia chafeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-254290/21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9913720-A1.
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The present sequence shows a high degree of similarity to the major antigenic protein 1 (MAPI) of Ehrlichia sp. The MAPI gene may be used in a vaccines to protect animals or humans against rickettsial diseases caused by a organisms of Rickettsial sp., Ehrlichia sp., Anaplasma sp. or Cowdria sp. The vaccine elicits an immune response protective against the rickettsial pathogen. The nucleic acid vaccines can be driven by the human cytomegalovirus (HCMV) enhancer-promoter. Cowdria ruminatium genes designated map 2, Ihworff, 4hworff, 18hworfl and 3gdorff may be used in therapeutic and diagnostic applications. The polypeptides are useful for detecting antibodies associated with used to detect the presence of rickettsial nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides useful as DNA vaccines for conferring immunity to rickettsial infection e.g. heartwater caused by Cowdria runinantium, comprises major antigenic protein 1 or 2 gene of rickettsial pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TC;
consist of proteins shown in AAY06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                    Gaps
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Alleman AR;
                                                                                                                                                                                                                                                                                                                                                                                                             Ehrlichia chaffeensis; VSA3; variable surface antigen 3; MAP1; major antigenic protein 1; antirickettsia1; vaccine; gene therapy; Rickettsia; Cowdria; Anaplasma; map2; Ihworf3; 4hworf1; 18hworf1;
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0
                                                                                                  Length 278;
                                                                                                                                  Indels
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Rurangirwa FR, Moreland AL, Simbi BH, Whitmire WW,
                                                                                                Score 97; DB 20;
Pred. No. 2.2e-08;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 97; DB 21;
Pred. No. 2.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                 Ehrlichia chaffeensis partial VSA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 44-45; 63pp; English.
                                                                                                                                                                                                                                                                                AAB36187 standard; Protein; 278 AA.
                                                                                                                                  0;
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100.0%;
                                                                                                Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 18; Conservative 0
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                                                                                                                                                                   1 NPTVALYGLKODWEGISS 18
                                                                                                                                                                                    60 nptvalyglkqdwegiss 77
                                                                                                                                                                                                                                                                                                                                                  02-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYFL ) UNIV FLORIDA.
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N-PSDB; AAC68704.
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Best Local Similarity
                                                 278 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200065063-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-APR-1999;
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AAB36187
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Matches

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AAU04197 RESULT

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The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in AAY06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAY06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                                                                                            Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel outer membrane proteins from Ehrlichia chaffeensis and Ehrlichia canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAP1 homologue; variable surface antigen; VSA4; rickettsia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 88; DB 20; Lenc
Pred. No. 7.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "putative signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
  AAY06945 standard; Protein; 280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW51094 standard; Protein; 280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ehrlichia chaffeensis VSA4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 13; Fig 5B; 55pp; English.
                                                                                                                                                                   E. chafeensis OMP-1C protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0059353.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US19600,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NPTVALYGLKQDWEGISS 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 nptvalyglkqdwngvsa 77
                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (OHIS ) UNIV OHIO STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohashi N, Rikihisa Y;
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                                                                                                                                                                                                                                                                                                                  Ehrlichia chafeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-254290/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         280 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAX34745
                                                                                                                                                                                                                                                                  detection; dog
                                                                                                                                                                                                                                                                                                                                                                           WO9913720-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-SEP-1998;
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                                                                                                                 05-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW51094;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
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     THE STATE OF THE S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence represents the amino acid sequence of variable surface antigen 3 (VSA3) isolated from Ehrlichia chaffeensis, which has similarity to major antigen protein (MAP). The MAP polynucleotides and polypeptides are useful as vaccines for conferring immunity to rickettsia infection, including Cowdria ruminantium causing heartwater. The MAP polynucleotides may be used as molecular markers in nucleic acid analysis procedures, and to produce the MAP polypeptides, which may be used to raise antibodies that are reactive with the polypeptides. The nucleic acids may further be used as probes to identify complementary sequences within other nucleic acid molecules or genomes, where such probes can be applied to identify or distinguish infectious strains of organisms in diagnostic procedures or in rickettsial research where identification of particular organisms or strains is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New MAP2 genes and polypeptides useful as vaccines for conferring immunity to human and animal rickettsial diseases, e.g. heartwater, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Major antigenic protein 1; MAP1; vaccine; immunogenic; rickettsia; infection; heartwater; diagnostic; variable surface antigen; VSA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Variable surface antigen 3 (VSA3) from Ehrlichia chaffeensis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nyika A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunity to human and animal rickettsial diseases, e.g. h
as molecular markers in nucleic acid analysis procedures
  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McGuire TC, Burridge MJ,
3M, Bowle MV, Alleman AR;
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100.0%; Pred. No. 2.2e-08;
ive 0; Mismatches 0;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Fig 2A-2B; 30pp; English.
                                                                                                                                                                                                                                                    AAU04197 standard; Protein; 278 AA.
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                                                     1 NPTVALYGLKQDWEGISS 18
                                                                                nptvalyglkqdwegiss 77
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                                                                                                                                                                                                                                                                                                                                                                     23-OCT-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barbet AF, Ganta RR, McC
Rurangirwa FR, Mahan SM,
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ehrlichia chaffeensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYFL ) UNIV FLORIDA.
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Matches 18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     278 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-OCT-1997;
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18;
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Gaps

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Indels

Sequence

Query Match

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Length 280;

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The present sequence shows a high degree of similarity to the major antigenic protein 1 (MAP1) of Ehrlichia sp. The MAP1 gene may be used in a vaccines to protect animals or humans against rickettsial diseases caused by a organisms of Rickettsia sp., Ehrlichia sp., Anaplasma sp. or Cowdria sp. The vaccine elicits an immune response protective against the rickettsial pathogen. The nucleic acid vaccines can be driven by the human cytomegalovirus (HCMV) enhancer promoter. Cowdria ruminatium genes designated map 2, Ihworf3, Ahworf1, 18hworf1 and 3gdorf3 may be used in therapeutic and diagnostic applications. The polypeptides are useful for detecting antibodies associated with infection by a rickettsial pathogen whilst the polynucleotides may be used to detect the presence of rickettsial nucleic acids.
                                                                                                                                                New polynucleotides useful as DNA vaccines for conferring immunity to rickettsial infection e.g. heartwater caused by Cowdria ruminantium, comprises major antigenic protein 1 or 2 gene of rickettsial pathogens
                      Barbet AF, Bowie MV, Ganta RR, Burridge MJ, Mahan SM, McGuire TC;
Rurangirwa FR, Moreland AL, Simbi BH, Whitmire WW, Alleman AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Major antigenic protein; MAP; vaccine; immunogenic; rickettsia; infection; heartwater; diagnostic; variable surface antigen; VSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Variable surface antigen 4 (VSA4) from Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 62; DB 21; Length 280;
Pred. No. 0.018;
4; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barbet AF, Ganta RR, McGuire TC, B
Rurangirwa FR, Mahan SM, Bowie MV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU04198 standard; Protein; 280 AA.
                                                                                                                                                                                                                                                           Claim 3; Page 45-46; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.9%;
60.0%;
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60 nttigvfglkgdwdg 74
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N-PSDB; AAS07578.
                                                                                    WPI; 2000-679675/66.
N-PSDB; AAC68705.
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Best Local Similarity
Matches 9; Conserv
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AAU04198
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                                                                                                                                                                                                                                                                                                                                                                                                                          This is the full-length variable surface antigen VSA4 protein of Ehrlichia chaffeensis. Its amino acid sequence was deduced from a partial open reading frame (ORF4) of a genomic locus (see AAV07179) of E. chaffeensis that was obtained on the basis of homology to the major antigenic protein MAPI (see AAM51088) of Cowdria ruminantium. This genomic locus included 5 ORF8 encoding similar, but non-identical protein (see AAM51091-95). A claimed composition comprises a nucleic acid (see AAW51076-82) encoding a polypeptide (see AAW5108-95). The number response against a rickettsial pathogen. The nucleic acid is used, in human or veterinary medicine, in vaccines to protect against Rickettsia, brilichia, Anaplasma and Cowdria species. The Ehrlichia antigenic associated with Ehrlichia infection (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                Composition containing nucleic acid encoding rickettsial antigen useful for, e.g. stimulating protective immune response in humans or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ehrlichia chaffeensis; VSA4; variable surface antigen 4; MAP1; major antigenic protein 1; antirickettsial; vaccine; gene therapy; Rickettsia; Cowdria; Anaplasma; map2; lhworf3; 4hworf1; 18hworf1; 3gdorf3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.9%; Score 62; DB 19; Length 280;
ilarity .60.9% pred. No. 0.018;
Conservative 4; Mismatches 2; Indels
                                                                                                                                                                         Ganta RR, Mahan SM, McGuire TC;
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                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Fig 2B; 39pp; English.
                                          97WO-US19044.
                                                                                  96US-0733230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-APR-2000; 2000WO-US10886.
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                                                                                                                                                                      Barbet AF, Burridge MJ,
Nyika A, Rurangirwa FR;
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60 nttigvfglkqdwdg 74
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                                                                                                                              (UYFL ) UNIV FLORIDA.
                                                                                                                                                                                                                                     WPI; 1998-251232/22.
N-PSDB; AAV07179.
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 AA;
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                                          17-OCT-1997;
                                                                                  17-OCT-1996;
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23-APR-1998
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Sequence

Best Loca Matches

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animals

AAB36188;

RESULT AAB36188

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Gaps

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New MAP2 genes and polypeptides useful as vaccines for conferring immunity to human and animal rickettsial diseases, e.g. heartwater, or as molecular markers in nucleic acid analysis procedures

(UYFL) UNIV FLORIDA.

22-APR-1999;

Nyika A;

S

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Gaps

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The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in AAY06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAY06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 59; DB 20; Length 288; Pred. No. 0.059; 3; Mismatches 3; Indels
                                                                          20; Length 280;
                                                                                                                                                 .;
                                                                      Score 59; DB 20;
Pred. No. 0.057;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY06959 standard; Protein; 288 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.8%;
60.0%;
                                                                          60.8%;
60.0%;
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Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                    Conservative
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                                                                                                                                                                                                                       1 NPTVALYGLKQDWEG 15
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60 ntttgvfglkqdwdg 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ohashi N, Rikihisa Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E. canis P30 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-254290/21
                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAX34759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ehrlichia canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ehrlichia canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detection; dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9913720-A1.
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AAY06942
ID AAY0
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                                                                                              The sequence represents the amino acid sequence of variable surface antigen 4 (VSA4) isolated from Ehrlichia chaffeensis, which has similarity to major antigen protein (MAP). The MAP polynucleotides and polypeptides are useful as vaccines for conferring immunity to rickettsia infection, including Cowdria ruminantium causing heartwater. The MAP polynucleotides may be used as molecular markers in nucleic acid analysis procedures, and to produce the MAP polypeptides, which may be used to raise antibodies that are reactive with the polypeptides. The nucleic acids may further be used as probes to identify or genomes, where such probes can be applied to identify or distinguish infectious strains of organisms in diagnostic procedures or in rickettsial research where identification of particular organisms or strains is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in ARV06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in ARV06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 62; DB 22; Length 280; Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
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                               Example 3; Fig 2A-2B; 30pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.9%;
60.0%;
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| 60 nttigvfglkqdwdg 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ehrlichia chafeensis.
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N-PSDB; AAX34748.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280 AA;
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Matches
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Gaps

McGuire TC;

Mahan SM,

Ganta RR,

us-09-765-739a-6.rag

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This is the near full-length variable surface antigen VSAS protein
of Ehrlichia chaffeensis; it lacks about 5-7 C-terminal amino acid
cresidues. The VSAS amino acid sequence was deduced from a partial
cresidues. The VSAS amino acid sequence was deduced from a partial
central state as obtained on the basis of homology to the major
antigenic protein MAPI (see AAN$1088) of Cowdria ruminantium. This
genomic locus included 5 ORFs encoding similar, but non-identical
proteins (see AAN$1091-95). A claimed composition comprises a
cucleic acid (see AAN$1076-82) encoding a polypeptide (see AAN$1088-99)
that elicits a protective immune response against a rickettsial
pathogen. The nucleic acid is used, in human or veterinary
medicine, in vaccines to protect against Rickettsia. Ehrlichia,
chaptagen and Cowdria species. The Bhrlichia antigenic
polypeptides can be used diagnostically to detect antibodies
ssociated with Ehrlichia infection (claimed).
                                                                                                   Composition containing nucleic acid encoding rickettsial antigen useful for, e.g. stimulating protective immune response in humans or
                                                                                                                                                  Claim 3; Fig 2B; 39pp; English.
                        Barbet AF, Burridge MJ,
Nyika A, Rurangirwa FR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYFL ) UNIV FLORIDA.
(UYFL ) UNIV FLORIDA.
                                                             WPI; 1998-251232/22.
N-PSDB; AAV07179.
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                 276 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200065063-A2
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                                                                                                                             animals
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  ó;
                                                                                                                                                                                                                                                                                                                                        The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and E. canis. The E. Chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in AAYO6943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAYO6959-97O. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                        canis; P30;
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0
                                                                                                                                                                                                                                                                         Novel outer membrane proteins from Ehrlichia chaffeensis and Ehrlichia canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 58; DB 20; Length 256;
Pred. No. 0.076;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAP1 homologue; variable surface antigen; VSA5; rickettsia; DNA vaccine.
                     Outer membrane protein; OMP; Ehrlichia chafeensis; E. detection; dog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ehrlichia chaffeensis VSA5 protein (partial sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1.25
/note= "putative signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW51095 standard; Protein; 276 AA
                                                                                                                                                                                                                                                                                                                 Claim 18; Fig 1; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.8%;
                                                                                                                                                             97US-0059353.
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E. chafeensis p28 protein
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                                                                                                                                                                                     (OHIS ) UNIV OHIO STATE.
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                                                                                                                                                                                                                Ohashi N, Rikihisa Y;
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                                                             Ehrlichia chafeensis
                                                                                                                                                                                                                                      WPI; 1999-254290/21.
N-PSDB; AAX34742.
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Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                 256 AA;
                                                                                    W09913720-A1
                                                                                                                                      18-SEP-1998;
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ID AAW5
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QQ
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Barbet AF, Bowie MV, Ganta RR, Burridge MJ, Mahan SM, McGuire TC;
Rurangirwa FR, Moreland AL, Simbi BH, Whitmire WW, Alleman AR;
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ehrlichia chaffeensis; VSA5; variable surface antigen 5; MAP1; major antigenic protein 1; antirickettsia!; vaccine; gene therapy; Rickettsia; Cowdria; Anaplasma; map2; lhworf3; 4hworf1; 18hworf1; 3gdorf3.
                                                              ö
Score 58; DB 19; Length 276;
Pred. No. 0.083;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                 AAB36189 standard; Protein; 276 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ehrlichia chaffeensis partial VSA5.
      59.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-APR-2000; 2000WO-US10886
                                                                                                                                           | || ::||||:|
59 nttvgvfglkqnwdg 73
                                                                                                            1 NPTVALYGLKQDWEG 15
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                                                                                                                                                                                                                 The present sequence shows a high degree of similarity to the major antigenic protein 1 (MAR1) of Ehrlichia sp. The MAP1 gene may be used in a vaccines to protect animals or humans against rickettsial diseases caused by a organisms of Rickettsia sp., Ehrlichia sp., Anaplasma sp. or Cowdria sp. The vaccine elicits an immune response protective against the rickettsial pathogen. The nucleic acid vaccines can be driven by the human cytomegalovirus (HCWV) enhancer-promoter. Cowdria ruminatium genes designated map 2, Ihworf3, 4hworf1, 18hworf1 and 3gdorf3 may be used in therapeutic and diagnostic applications. The polypeptides are useful for detecting antibodies associated with infection by a rickettsial pathogen whilst the polynucleotides may be used to detect the presence of rickettsial nucleic acids.
                                              New polynucleotides useful as DNA vaccines for conferring immunity to rickettsial infection e.g. heartwater caused by Cowdria ruminantium, comprises major antigenic protein 1 or 2 gene of rickettsial pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heartwater, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence represents the amino acid sequence of variable surface antigen 5 (VSA5) isolated from Ehrlichia chaffeensis, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New MAP2 genes and polypeptides useful as vaccines for conferring immunity to human and animal rickettsial diseases, e.g. heartwaten as molecular markers in nucleic acid analysis procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wajor antigenic protein; MAP; vaccine; immunogenic; rickettsia; infection; heartwater; diagnostic; variable surface antigen; VSA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Variable surface antigen 5 (VSA5) from Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21; Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nyika A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burridge MJ,
Alleman AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 58; DB 21;
Pred. No. 0.083;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McGuire TC, B
M, Bowie MV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Fig 2A-2B; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU04199 standard; Protein; 276 AA.
                                                                                                                                                                       Claim 3; Page 47; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.8%;
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R, Mahan SM,
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Best Local Similarity 60.0.
Section 9; Conservative
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59 nttvgvfglkqnwdg
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N-PSDB; AAS07578.
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N-PSDB; AAC68706
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has similarity to major antigen protein (MAP). The MAP polynucleotides and polypeptides are useful as vaccines for conferring immunity to rickettsia infection, including Cowdria ruminantium causing heartwater. The MAP polynucleotides may be used as molecular markers in nucleic acid analysis procedures, and to produce the MAP polypeptides, which may be used to raise antibodies that are reactive with the polypeptides. The nucleic acids may further be used as probes to identify complementary sequences within other nucleic acid molecules or genomes, where such probes can be applied to identify or distinguish infectious strains of organisms in diagnostic procedures or in rickettsial research where identification of particular organisms or strains is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This polypeptide comprises the major antigen protein 1 gene (MAP1) of Ehrlichia chaffeensis. It is encoded by the MAP1 gene (see AAV07177). A claimed composition comprises a nucleic acid (see protective immune response against a rickettsial pathogen. The nucleic acid is used, in human or veterinary medicine, in vaccines to protect against Rickettsia, Ehrlichia, Anaplasma and Cowdia species. The nucleic acid does not replicate in the host but remains episomal and capable of expressing polypeptide for at least 19 mth. The Ehrlichia antigenic polypeptides can be used aingnostically to detect antibodies associated with Ehrlichia infection (claimed).
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Composition containing nucleic acid encoding rickettsial antigen useful for, e.g. stimulating protective immune response in humans or
                                                                                                                                                                                                                                                                                                                                          ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAP1 gene; major antigenic protein 1; rickettsia; DNA vaccine.
                                                                                                                                                                                                                                                                                                    DB 22; Length 276; 0.083;
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                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ehrlichia chaffeensis major antigenic protein 1 (MAP1).
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Pred. No. 0.083
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW51089 standard; Protein; 280
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                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                             1 NPTVALYGLKQDWEG 15
                                                                                                                                                                                                                                                                                                                                                                                                                73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYFL ) UNIV FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                59 nttvgvfglkqnwdg
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-251232/22.
                                                                                                                                                                                                                                              276 AA;
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XX SQ Sequence 280 AA;

Query Match 59.8%; Score 58; DB 19; Length 280; Best Local Similarity 60.0%; Pred. No. 0.084; Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps

0;

1 NPTVALYGLKQDWEG 15 | | | ::||||:|| 60 nttvgvfglkqnwdg 74

Db δ

Search completed: March 14, 2002, 09:09:38 Job time: 429 sec

us-09-765-739a-7.rspt

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092gjl ehrlichia c
09f475 ehrlichia c
052106 ehrlichia c
03af99 cowdria rum
09af98 cowdria rum
046321 cowdria rum
046321 cowdria rum
046332 cowdria rum
09af6 cowdria rum
09af1 cowdria rum
09af2 cowdria rum
09af31 cowdria rum
09sf01 cowdria rum
09sf13 arabidopsis
005352 cowdria rum
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Rickettsiaceae; Ehrlichiaae; Ehrlichia.
NCBI_TaxID=945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-ARANSAS;

X MEDLINE-98084465; Pubmed-9423849;
X MEDLINE-98084465; Pubmed-9423849;
X Obasah; N., Zhang Y., Rikihisa Y.;
A Chasah; N., Zhang Y., Rikihisa Y.;
T "Immunodominant major outer membrane proteins of Ehrlichig T are encoded by a polymorphic multigene family.";
T infect: Lumun. 66:132-139(1988).
R EMBL: U72291; AAC02940.1;
R Pfan; PFO161; Surface-Aq_2;
R Pfan; PFO161; Surface-Aq_2;
C SEQUENCE 280 AA; 30731 MW; CCAA6C34E2AF393E CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            085357 PRELIMINARY; PRT; 280 AA. 085357; 01-NOV-1998 (TrEMBLrel. 08, Created) 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
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ilarity 100.0%; Pred. No. 8.6e-09;
Conservative 0; Mismatches 0;
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Q06352
Q9U993
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09F475
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09S6H0
085360
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                             OMP-1F.
Ehrlichia chaffeensis.
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085357 ehrlichia c
092732 ehrlichia c
085817 ehrlichia c
085378 ehrlichia c
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092009 ehrlichia c
09473 ehrlichia c
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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sp_nwertebrate;

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sp_organelle;
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sp_vertebrate:*
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Maximum DB seq length: 2000000000
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us-09-765-739a-7.rspt

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Q9RH35 PRELIMINARY; PRT; 246 AA.
Q9RH35, 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
00TER MEMBRANE PROTEIN P28 PRECURSOR (FRAGMENT).
Ehrlichia chaffeensis.
Bacteria: Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae, Ehrlichieae; Bhrlichia.
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085817;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Ehrlichia chaffeensis.
Ehrlichia chaffeensis.
RICHELTS Proteobacteria; alpha subdivision; Rickettsiales;
RICKettsiaceae; Ehrlichieae; Ehrlichiae.
                                                                                                 Length 288;
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                                                                                            Score 96; DB 2; Length 288
Pred. No. 1.2e-07;
1; Mismatches 0; Indels
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Yu.X.-J., Walker D.H.;
Webrisch achaffeensis 28 kDa outer membrane protein.";
Submitted (Jul-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF077734; AAC31547.1;
Interpro; IPR002566; Surface_A9_msp4.
Pfam: PF01617; Surface_A9_2.1.
SEQUENCE 276 AA; 30027 WW; 2FD3698FCFIF60BE CRC64;
     Pfam; PF01617; Surface_Ag_2; 1.
SEQUENCE 288 AA; 31590 MW; 86DCAECB88E9BF5E CRC64;
                                                                                              Query Match 93.2%;
Best Local Similarity 94.4%;
Matches 17; Conservative
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STRAIN=SAPULPA;
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MEDLINE-98321180; PubMed-9647746;
Reddy G.R., Sulsona C.R., Barbet A.F., Mahan S.M., Burridge M.J.,
Alleman A.R.;
Molecular characterization of a 28 kDa surface antigen gene family of
the tribe Ehrlichiae.";
EMBL, ARC5701201;
LINCHER, RO62701;
LINCHER, Surface, Ag_msp4.
FROM: PF0015 Surface, Ag_msp4.
FROM: PRO015 Surface, Ag_msp4.
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STRAIN-OKLAHONA,
MEDLINE-98371112; PubMed-9705412;
MEDLINE-98371112; PubMed-9705412;
MEDLINE-98371112; PubMed-9705412;
MISTORY OF A., Zhi N., Rikihisa Y.;
"Cloning and characterization of multigenes encoding the immunodominant 30-kilodalton major outer membrane proteins of Ehrlichia canis and application of the recombinant protein for Ehrlichia canis and application of the recombinant protein for
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"A conserved, transcriptionally active p28 multigene locus of Ehrlichia canis."
Gene 254:245-252(2000).
EMBL, AR078553, AAC8667.1; -.
EMBL, AR078744; AAC8667.1; -.
InterPro; IPR002566; Surface_Ag_msp4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U. MAY-1999 (TrEMBLrel. 10, Created)
U. MAY-1999 (TrEMBLrel. 10, Last sequence update)
U. MAY-1999 (TrEMBLrel. 10, Last sequence update)
U. JUN-2001 (TrEMBLrel. 17, Last annotation update)
30-KDA MAJOR OUTER MEMBRANE PROTEIN (P28-8).
BJO OR P28-8.
BAIL (All a canis.
BACTETIA; Proteobacteria; alpha subdivision; Rickettsiales; NCBL Transleyed; Ehrlichieae; Ehrlichia.
01.JUN-2001 (TrEMBLrel. 17, Last annotation update)
EN IDA MAJOR SURFACE ANTIGEN-4.
ENTLICHE chaffeensis.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaccee; Entlichieae; Ehrlichia.
NGBL_TaxID-945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 280;
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J. Clin. Microbiol. 36:2671-2680(1998).
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MEDLINE=20432107; PubMed=10974556;
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Best Local Similarity 94.75
Matches 18; Conservative
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MEDLINE-21153356; PubMed-11254561;
Ohashi N., Rikihisa Y., Unver A.;
"Analysis of Transcriptionally Active Gene Clusters of Major Outer
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Rickettsiaceae, Ehrlichieae; Ehrlichia.
NCBL_TaxID=945;
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Rickettsiaceae; Ehrlichieae; Ehrlichia.
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84.2%; Pred. No. 2.3e-06;
Eive 1; Mismatches 2; Indels
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Infect. Immun. 69:2083-2091(2001).
EMBL: U72291. AAR28673.1; -.
SEQUENCE 281 AA. 30343 MW, A99E5F7C4459AA9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 Yu.X.-J., Walker D.H.;
"Ehrlichia chaffeensis 28 kDa outer membrane protein.";
"Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AR077733; ARC31546.1;
"InterPro: IFR002566; Surface_Ag_msp4.
Pfam; PF01617; Surface_Ag_2; 1.
SEQUENCE 280 AA; 30304 MW; 91C54AC7851B77F2 CRC64;
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84.2%; Pred. No. 2.3e-06;
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Ohashi N., Zhi N., Zhang Y., Rikihisa Y.;
Immunodominant major outer membrane proteins of
are encoded by a polymorphic multigene family.";
Infect. Immun. 66:132-139(1998).
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01-JUN-2001 (TrEMBLrel. 17, Last
01-JUN-2001 (TrEMBLrel. 17, Last
MAJOR OUTER MEMBRANE PROTEIN P28.
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                  Best Local Similarity
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Best Local Similarity
Matches 16; Conserv
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SEQUENCE FROM N.A.
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Biochem Biophys. Res. Commun. 247:636-643(1998).
EMBL: AF062761; AAC27616.1;
InterPro: IPR002566; Surface_Ag_msp4.
Pfam: PF01617; Surface_Ag_2; 1.
                                                                                     Gaps
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BEDLINE-98321180; PubMed=9647746;
Reddy G.R., Sulsona C.R., Barbet A.F., Mahan S.M., Burridge M.J.,
Alleman A.R.;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 17, Last annotation update)
28 KDA MAJOR SURFACE ANTIGEN-5 (FRAGMENT).
Entlichia chaffeensis.
Bacteria, Proteobacteria; alpha subdivision; Rickettsiaceae, Ehrlichiaee; Ehrlichiae.
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Bacteria, proteobacteria, alpha subdivision, Rickettsiales,
Rickettsiaceae; Ehrlichieae; Ehrlichia.
NCBI_TaxID=945;
                                                    Length 276;
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84.2%; Pred. No. 2.3e-06;
.ive 1; Mismatches 2; Indels
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"Ehrlichia chaffeensis 28 kDa outer membrane protein.";
"Ehrlichia (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF077732; AAC31545.1;
InterPro; IPR002566; Surface_Ag_msp4.
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2;
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01-NOV-1998 (TrEMBLrel. 08, Created)
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OUTER MEMBRANE PROTEIN P28 PRECURSOR.
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                                                  86.4%;
88.9%;
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Matches 16; Conservative
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Best Local Similarity
Matches 16; Conserv
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Ehrlichia chaffeensis

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Length 280;

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STRAINCECANDOMA;
MEDLINE-21153566; Pubmed-11254561;
Ohashi N., Rikihisa Y., Univer A.;
"Analysis of Transcriptionally Active Gene Clusters of Major Outer
Membrane Protein Multigene Family in Ehrlichia canis and E.
chaffeensis.";
Ohashi N., Unver A., Zhi N., Rikihisa Y.;
"Cloning and characterization of multigenes encoding the immunodominant 30 *Kliodalton major outer membrane proteins of Ehrlichia canis and application of the recombinant protein for Serodiagnosis.";
J. Clin. Microbiol. 36:2671-2680(1998).
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 77.7%; Score 80; DB 2; Length 280 Best Local Similarity 73.7%; Pred. No. 4.6e-05; Matches 14; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                        chaffeensis.";
Infect. Immun. 69:2083-2091(2001).
EMBL: AF078553: AAK28699.1, -.
SEQUENCE 280 AA; 30803 MW; 27238BEIC7E68A91 CRC64;
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59 NSTVGVFGLKHDWNGGTIS 77
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SEQUENCE FROM N.A.
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MEDLINE-99242757; PubMed-10225842;
MCBLINE-99242757; Walker D.H.;
MCBRIGG J.W., Yu, Xi, Walker D.H.;
MOHOGULIAR Cloning of the gene for a conserved major immunoreactive
28-kilodalton protein of Ehrlichia canis: a potential serodiagnostic
                                                                                         Gaps
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Bacteria: Proteobacteria: alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
NCBL_TaxID=944;
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Rickettsiacceae; Bhrlichieae; Bhrlichia.
NCBL_TaxID=944;
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MCBLINE-20422107.
MCBLINE-20422107.
MCBLIGG J.W., YU X.J., Walker D.H.;
MA conserved, transcriptionally active p28 multigene locus
EMBLICHIA canis.'
Gene 254:245-252(2000).
EMBL: AF087744; AAG14361.1; -
Interpro: IPR002566; Surface_Ag_msp4.
Pfam: PP01017; Surface_Ag_2; 1.
SEQUENCE 280 AA; 30762 MW; BE284A4B94FE3123 CRC64;
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                                            Length 281;
                                            85.4%; Score 88; DB 2; Length 281
84.2%; Pred. No. 2.3e-06;
ive 1; Mismatches 2; Indels
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MAJOR OUTER MEMBRANE PROPERN P30-2.
                                                                                                                                                                                                                                                                                      280 AA.
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MEDLINE=98371112; PubMed=9705412;
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                                               Query Match 85.4
Best Local Similarity 84.2
Matches 16; Conservative
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Matches 14; Conserv
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SEQUENCE FROM N.A.
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Q9F473
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MEDINE-9804465; Pubmed-9423849;
MEDINE-9804465; Pubmed-9423849;
Obtashi N., Zhi N., Zhang Y., Rikihisa Y.;
"Immunodominant major outer membrane proteins of Ehrlichia chaffeensis are encoded by a polymorphic multigene family.";
Infect. Immun. 66:132-139(1998).
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Reddy G.R., Sulsona C.R., Barbet A.F., Mahan S.M., Burridge M.J.,
Alleman A.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                Ehrlichia chaffeensis.
Bacteria, Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
NCBL_TaxID=945;
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286 AA; 31509 MW; F145A79270F386BE CRC64;
                                                 Created)
Last sequence update)
Last annotation update)
              286 AA.
              PRT;
052105 PRELIMINARY;
052105;
01-JUN-1998 (TrEMBLrel. 06, C:
01-JUN-1998 (TrEMBLrel. 06, Le
01-JUN-2001 (TrEMBLrel. 17, Le
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Ehrlichia canis.
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SEQUENCE
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RESULT 15
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MCBride J.W., Yu X.J., Walker D.H.;
McBride J.W., Yu X.J., Walker D.H.;
"Molecular cloning of a conserved major immunoreactive 28-kilodalton protein gene from a polymorphic multiple gene family of Ehrlichia canis.";
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 17, Last annotation update)
28 KDA OUTER MEMBRANE PROTEIN (FRAGMENT).
Burlichia canis.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
                                                                                                              Ehrlichia canis.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
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                                                                                                                                                                                                                                                         Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AF082745: AAC64551.1; -...
InterPro; IPR002566; Surface_Ag_msp4.
Pfam; PF01617; Surface_Ag_2; 1.
NON_FER 278 278
SEQUENCE 278 AA; 30485 MW; 697CB6CA413BBA68 CRC64;
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InterPro; IPR002566; Surface_Ag_msp4.
Pfam; PF01617; Surface_Ag_2; 1.
NON TER 278 278
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U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
28 KDA OUTER MEMBRANE PROTEIN (FRAGMENT).
                                    278 AA.
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61 STVGVFGLKHDWDGSPI 77
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Best Local Similarity 76.5
Matches 13; Conservative
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                                    PRELIMINARY;
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STRAIN=DEMON (NORTH CAROLINA);
MCBride J.W., Yu X.J., Walker D.H.;
"Molecular cloning of a conserved major immunoreactive 28-kilodalton protein gene from a polymorphic multiple gene family of Ehrlichia canis.";
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Rickettsiaceae; Ehrlichieae; Ehrlichia.
NCBL_TaxID=944;
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76.5%; Pred. No. 0.00062;
Live 1; Mismatches 3; Indels
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                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
28 KDA OUTER MEMBRANE PROTEIN (FRAGMENT).
278 AA.
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Best Local Similarity 76.5%
Matches 13; Conservative
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4: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/laa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/laa/PcTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	Sequence	Sednence	Sednence	Seguence	Sequence	Sequence	Seguence	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
SUMMARIES	-953-	-953-	-733-	-953-	3-953-326-15	53-	(1)	3-953-326-2	(+)	3-446-600A-4	US-08-304-309-2	3-991-942-2	US-09-138-103-2	PCT-US95-04567-4	US-08-304-309-4	US-08-991-942-4	PCT-US95-04567-2	US-08-586-165-3	3-586-165-5	US-08-053-614-2	US-08-316-397B-2	US-09-034-306-2	US-09-259-437-2	-US93-09782-2	3-053-614-4	-08-316-397B-4	09-034-306-4
S	ns-o	0S-08	0S-08	us-08	us-08-	us-0	US-08-7	US-08-95	US-08-95	US-08-44	ns-0	ns-0	ns-0	PCT-1	ns-0	0S-08	PCT-1	0S-08	0S-08	0S-08	0S-0	0S-0	ns-0	PCT-1	US-08	ns-08	ns-0
DB	4.	4	m ·	4	4	4	m	4	4	٦	7	٣	4	Ŋ	~	က	Ŋ	က	m	Н	۲	7	4	S	, -1	Н	~
% Query Match Length	280	276	280	280	286	278	287	287	133	135	1025	1025	1025	1025	1025	1025	1025	371	372	859	859	859	859	859	1181	1181	1181
% Query Match	94.2	85.4	ഗ	'n.	71.8	58.3	57.8	57.8	53.4	39.8	38.8	38.8	38.8	38.8	37.9	37.9	37.9	36.9	36.9	36.9	36.9	36.9	36.9	36.9	36.9	36.9	36.9
Score	97	88	88	88	74		59.5	o,	52	41	40	40	40	40	39	39	39	38	38	38	38	38	38	38	38	38	38
Result No.		7	ω.	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

PCT-US-23-43/1-4 Seque US-09-23-43/1-4 Seque US-08-947-823-3 Seque US-08-947-823-5 Seque US-08-190-8024-173 Seque US-08-190-8024-173 Seque US-08-190-8024-173 Seque US-08-190-8024-173 Seque US-08-190-8024-27 Seque US-08-190-8024-47 Seque US-08-190-8024-47 Seque US-08-190-8024-47 Seque US-08-190-8024-47 Seque US-08-477-346-47 Seque US-08-953,326	Length 280 ; Indels
RESULT RESULT APPLICANT: Barber, Anthony F. APPLICANT: McGuire, Travisc C. APPLICANT: Mahan, Suman M. TITLE OF INVENTION: Nuclease 10-17 TITLE OF INVENTION: Nuclease 10-17 TITLE OF INVENTION: Nuclease 10-17 FERRIFER APPLICATION NUMBER: US, EARLIFER APPLICATION NUMBER: US, EARLIFER PFILLING DATE: 1997-10-17 FERRIFER FFILLENT DATE: 1997-10-17	733,230 score 97; DB 4; Pred. No. 1.4e-08; Mismatches 1 3326

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APPLICANT: Mahan, Suman M.

TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
FILE REFERENCE: UF-16701
CURRENT APPLICATION NUMBER: US/08/953,326
EARLIER APPLICATION NUMBER: 08/953,326
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PLENCH DOS: 24
SOFTWARE: PLENCH DATE: 20
EARLIER PLENCH DOS: 24
SOFTWARE: PLENCH DATE: 20
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Sequence 4, Application US/08733230

Fatent No. 602538

GENERAL INFORMATION:
APPLICANT: Barbet, Anthony F.
APPLICANT: Ganta, Roman Reddy
APPLICANT: Buridge, Michael J.
APPLICANT: Will Aceme
APPLICANT: Will Aceme
APPLICANT: Will Aceme
APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Rickettsial Diseases and Methods of Use
CORRESPONDENCES: 6 CORRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STATE: 12-10 N. W. 41st Street, Suite A-1
CITY: Galnesville
CONFURE: FLO
COUNTRY: USA
COMPUTER: EMP PC Compatible
COMPUTER: EMP PC Compatible
COMPUTER: EMP PC Compatible
COMPUTER: Bandesville
COMPUTER: Bandesville
COMPUTER: Bandesville
COMPUTER: Bandesville
COMPUTER: Callow NUMBER: US/08/733,230
FILIN DATE
CLASSIFICATION NUMBER: 36,965
REGISTRATION NUMBER: 36,965
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF-167
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NOW. 4.
INFORMATION FOR SPC 710 NOW. 4.
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85.4%; Score 88; DB 4; Length 276
Best Local Similarity 84.2%; Pred. No. 4.3e-07;
Matches 16; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Ehrlichia chaffeensis
US-08-953-326-18
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 280 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NTTTGVFGLKQDWDGSTIS 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-733-230-4
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US-08-733-230-4
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US-UB-93-324-4
US-UB-93-324-4
US-UB-93-324-4
Datent No. 621872
GENERAL INFORMATION:
APPLICANT: Barbet, Anthony F.
APPLICANT: Barta, Roman R.
APPLICANT: Burridge, Michael J.
APPLICANT: Burridge, Michael J.
APPLICANT: Wahan, Suman M.
TITLE OF INVENTION: NUCleic Acid Vaccines Against Rickettsial Diseases of TITLE OF INVENTION: NUCleic Acid Vaccines Against Rickettsial Diseases of TITLE OF INVENTION: NUCleic Acid Vaccines Against Rickettsial Diseases of TITLE OF INVENTION: NUCLEic Acid Vaccines Against Rickettsial Diseases of TITLE OF INVENTION: NUMBER: US/08/953,326
CURRENT FILING DATE: 1997-10-17
CURRENT FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/733,230
EARLIER PILING DATE: 1996-10-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTHEN 200
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Sequence 15, Application US/08953326
Fatent No. 6551872
GENERAL INFORMATION:
APPLICANT: Barbet, Anthony F.
APPLICANT: Ganta, Roman R.
APPLICANT: Buridge, Michael J.
APPLICANT: Buridge, Michael J.
APPLICANT: Buridge, Michael J.
APPLICANT: Buridge, Michael J.
APPLICANT: Wahan, Suman M.
APPLICANT: Wahan, Suman M.
APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of TITLE OF INVENTION: Animals and Humans
FILE REPERENCE: UP-167C1
CURRENT APPLICATION NUMBER: US/08/953,326
CURRENT APPLICATION NUMBER: US/953,326
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-17
SERLIER FILING DATE: 1997-10-17
SERLIER FILING DATE: 1997-10-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
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                                                     Gaps
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     Length 280;
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Pred. No. 4.3e-07;
1; Mismatches 2; Indels
Score 88; DB 3; Length 280
Pred. No. 4.3e-07;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT; ORGANISM: Ehrlichia chaffeensis
US-08-953-326-4
  Query Match 85.4%;
Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 85.4%;
Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                       1 NTTTGVFGLKQDWDGSTIS 19
                                                                                                                                    60 NTTVGVFGLKQNWDGSAIS 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NTTTGVFGLKQDWDGSTIS 19
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US-08-953-326-15
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GENERAL INFORMATION:
APPLICANT: Barbet, Anthony F.
APPLICANT: Ganta, Roman R.
APPLICANT: Ganta, Roman R.
APPLICANT: McGuire, Travis C.
APPLICANT: Burridge, Michael J.
APPLICANT: Nyika, Aceme
APPLICANT: Rurandirwa, Fred R.
APPLICANT: Rurandirwa, Fred R.
APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
FILE REFERENCE: UF-167C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 0.024;
1; Mismatches 1; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.8%; Score 59.5; DB 3; Length 287; 80.0%; Pred. No. 0.024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/733,230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/08/953,326
CURRENT FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/953,326
EARLIER FILING DATE: 1997-10-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: 08/733,230
                                                                                            COMPUTER READABLE FORM:
MBDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 514
ATTORNEY-AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFREENCE/DOCKET NUMBER: UF-16
TELECHMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-375-8100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 287 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08953326
Patent No. 6251872
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NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
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80.0%;
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US-08-953-326-2
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Best Local Similarity 80.0%
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Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-733-230-2
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     Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                             COUNTRY: US
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US-08-953-326-2
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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16, Application US/08953326

Sequence 16, Application US/08953326

GENERAL INFORMATION:
APPLICANT: Barbet, Anthony F.
APPLICANT: Genta, Roman R.
APPLICANT: Genta, Roman R.
APPLICANT: Buridge, Michael J.
APPLICANT: Buridge, Michael J.
APPLICANT: Nurangirue, Fred R.
APPLICATION NUMBER: 08/953,326
EARLIER APPLICATION NUMBER: 08/953,326
EARLIER PILING DATE: 1997-10-17
EARLIER PILING DATE: 1997-10-17
EARLIER PILING DATE: 1996-10-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
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Patent No. 6025338

GENERAL INFORMATION:
APPLICANT: Barbet, Anthony F.
APPLICANT: Ganta, Roman Reddy
APPLICANT: Burridge, Michael J.
APPLICANT: Rurangirwa, Fred R.
APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Nucleic Acid Vaccines Against
TITLE OF INVENTION: Rickettsial Diseases and Methods of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 58.3%; Score 60; DB 4; Length 278; Best Local Similarity 52.6%; Pred. No. 0.019; Matches 10; Conservative 4; Mismatches 5; Indels
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STREET: 2421 N.W. 41st Street, Suite A-1
                                             ; TYPE: PRT
; ORGANISM: Ehrlichia chaffeensis
US-08-953-326-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Ehrlichia chaffeensis
US-08-953-326-16
                                                                                                                                                                                                                                                                1 NTTTGVFGLKQDWDGSTIS 19
                                                                                                                                                                                                                                                                                              60 NTTVGVFGIEQDWDRCVIS 78
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                                                                                                                                                                                                                  Conservative
                                                                                                                                                              Query Match
Best Local Similarity
Matches 13; Conserv
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SEQ ID NO 15
LENGTH: 286
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US-08-304-309-2
Sequence 2, Application US/08304309
Fatent No. 585454
GENERAL INFORMATION:
APPLICANT: GENERALIAN GENERALIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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Pred. No. 1.9e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
39.8%; Score 41; DB 1; Length 135;
Best Local Similarity 47.6%; Pred. No. 12;
Matches 10; Conservative 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: CALILOLING
COUNTRY: US
ZIP: 94105-1493

ZIP: 94105-1493

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAFA:
APPLICATION NUMBER: US/08/304,309
FILING DATE: 09-SEP-1994
CLASSIFICATION: USBP-1994
CLASSIFICATION: 135
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REFERENCE/DOCKET NUMBER: 15.280-210
TELECOMMUNICATION INFORMATION:
MET FORMORY CONTROL AS A 2 2 6 6 0 0
                                                         REFERENCE/DOCKET NUMBER:
TELECHMUNICATION INFORMATION:
TELEPHONE: (513) 651-6128
TELEFAX: (513) 651-6941
TELEFAX: (213) 651-6941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
   NAME: Ann G. Robinson
REGISTRATION NUMBER: 39,820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INPORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 1025 amino acids
TYPPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 38.8%;
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: Linear;
MOLECULE TYPE: Protein
US-08-446-600A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-08-304-309-2
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                                                                                                                                                                                                                                                                                                                      TYPE: Amino Acid
                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
US-08-953-326-20
Sequence 20, Application US/08953326
Sequence 20, Application US/08953326
Sequence 20, Application US/08953326
Sequence 20, Sequence 20, Application US/08953326
SEMERAL INFORMATION:
APPLICANT: Barbet, Anthony F.
APPLICANT: Ganca, Roman R.
APPLICANT: Mathan R.
APPLICANT: Within APPLICANT: Wathan Mucleic Acid Vaccines Against Rickettsial Diseases of TITLE OF INVENTION: Mucleic Acid Vaccines Against Rickettsial Diseases of TITLE OF INVENTION: Animals and Humans
TITLE OF INVENTION: Animals and Humans
TITLE OF INVENTION: Mumber: US/08/953,326
CURRENT FILING DATE: 1997-10-17
SEARLIER FILING DATE: 1997-10-17
SEARLIER FILING DATE: 1996-10-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE PATEUT VET. 2.0
SEQ ID NO 20
LENGTH: 133
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Pred. No. 0.055;
3; Mismatches 4; Indels
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COUNTRY: USA
ZIP: 45202-4182
COMPUTER READBALE FORM:
MEDIUW TYPE: DISKette, 3.5 inch, 720 Kb storage COMPUTER: EIDE COMPUTER: DESKETE, MS-DOS
SOFTWARE: WORDFAILE: MS-DOS
SOFTWARE: WORDFR: 20.5
CURRENT APPLICATION DATA:: 24 May 1995
FILING DATE: 24 May 1995
CLASSIFICATION NUMBER: US/08/940,513
APPLICATION NUMBER: PGT/US93/1139
FILING DATE: 24 No. 5719126ember 1992
FILING DATE: 24 No. 5719126ember 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 53.4%;
Best Local Similarity 58.8%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT; ORGANISM: Ehrlichia canis
US-08-953-326-20
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Gaps
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Pred. No. 1.9e+02;
2; Mismatches 3; Indels
                                                                                                                                                38.8%; Score 40; DB 4; Length 1025; 58.3%; Pred. No. 1.9e+02;
                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: DIHYDROPYRIMIDINE DEHYDROGENASE TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTE: Texas
COUNTRY: United States of America
ZITE: 7210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version
SOFTWARE: PAT.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04567
FILING DATE: CONCURRENTLY HEREWITH
                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UOAB025P--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US 08/227,357
                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application PC/TUS9504567
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: UF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (713) 789-26/9
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 38.8%;
Best Local Similarity 58.3%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1025 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 13-APR-19
CLASSIFICATION:
                                                                                                                                                                       Best_Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein PCT-US95-04567-4
                                          TYPE: PRT ORGANISM: Homo sapiens US-09-138-103-2
                                                                                                                                                                                                                                                                736 NTVSGLMGLKSD 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      736 NTVSGLMGLKSD 747
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                                                                                                                                                                                                                                                                                                                                           RESULT 14
PCT-US95-04567-4
                      LENGTH: 1025
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US-08-304-309-4
    SEQ ID NO 2
                                                                                                                                                Query Match
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APPLICANT: Yoshikubo, Takashi
APPLICANT: Yoshikubo, Takashi
APPLICANT: Wasami
TITLE OF INVENTION: Immunological Materials and Methods for Detecting
TITLE OF INVENTION: Immunological Materials and Methods for Detecting
TITLE OF INVENTION: Dihydropyrimidine Dehydrogenase
FILE REFERENCE: 09/138,103 Yoshikubo, et al.
CURRENT APPLICATION NUMBER: US/09/138,103A
EARLIER APPLICATION NUMBER: 97114630.3
EARLIER PILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                APPLICANT: GONZALEZ, Frank J.
APPLICANT: GONZALEZ, Frank J.
APPLICANT: FERNANDEZ-SALGUERO, PEDRO
TITLE OF INVENTION: CLONING AND EXPRESSION OF CDNA FOR HUMAN
TITLE OF INVENTION: DIHYDROPYRIMIDINE DEHYDROGENASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 3; Length 1025;
Pred. No. 1.9e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                               ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Streuart Street Tower, One Market Plaza CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/304,309
FILING DATE: 09-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: SMITh, Timothy L.
REGISTRATION NUMBER: 35,367
FELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LEAGHT: 1025 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09138103A Patent No. 6232448
                                                       RESULT 12
US-08-991-942-2
Sequence 2, Application US/08991942
Patent No. 6015673
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.8%;
58.3%;
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Matches 7; Conservative
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736 NTVSGLMGLKSD 747
736 NTVSGLMGLKSD 747
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ZIP: 94105-1493
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US-09-138-103-2
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Sequence 4, Application US/08304309
Patent No. 5854544
SENERAL INFORMATION:
APPLICANT: GONZALEZ_FIRE J.
APPLICANT: FERNANDEZ_SALGUERO, PEDRO
TITLE OF INVENTION: DIMYDROPRIMIDINE DEHYDROGENASE
NUMBER OF SEQUENCES: 1
STATE: California
COUNTRY: San Francisco
STRREY: San Francisco
COUNTRY: US
STATE: California
COUNTRY: US
STATE: California
COMPUTER READABLE PORM:
MEDIUM TYPE: IBPP C compatible
OPERATING SYSTEM: PC compatible
OPERATING SYSTEM: PC compatible
OPERATING SYSTEM: DS/080/304,309
FILING DATE: US/08/204,309
FILING DATE: US/08-1994
CLASSIFICATION NUMBER: 15280-210
FREISTRATION NUMBER: 15280-210
FREISCAMTUNICATION INFORMATION:
NAME: Smith, Timothy L.
SEQUENCE CHARACTERISTICS:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION PROPRATIOS:
TELECOMMUTICATION PROPRATION:
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Search completed: March 14, 2002, 09:07:42 Job time: 843 sec

|| :|: ||| | 736 NTVSGLMGLKAD 747 1 NTTTGVFGLKQD 12

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March 14, 2002, 09:09:38 ; Search time 111.55 Seconds
(without alignments)
12.617 Million cell updates/sec
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SIDB8/gcgdata/geneseqg/AA1989.DAT:
SIDB8/gcgdata/geneseqg/AA1999.DAT:
SIDB8/gcgdata/geneseqg/AA1992.DAT:
SIDB8/gcgdata/geneseqg/AA1992.DAT:
SIDB8/gcgdata/geneseqg/AA1993.DAT:
SIDB8/gcgdata/geneseqg/AA1995.DAT:
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SIDB8/gcgdata/geneseqg/AA1995.DAT:
SIDB8/gcgdata/geneseqg/AA1999.DAT:
SIDB8/gcgdata/geneseqg/AA1999.DAT:
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/SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDS8/gcgdata/geneseqp/AA1982.DAT:*
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/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             522463 segs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                 103
1 NTTTGVFGLKQDWDGSTIS 19
                                                                                                                                                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                  US-09-765-739A-7
                                                                                                                                                                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                Sednence:
                                                                                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                     Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	E. chafeensis OMP-	Ehrlichia chaffeen	Ehrlichia chaffeen	Variable surface a	E. canis P30 prote	E. chafeensis p28	Ehrlichia chaffeen	Ehrlichia chaffeen	Variable surface a	Ehrlichia chaffeen	Ehrlichia chaffeen
	ID	AAY06948	AAW51094	AAB36188	AAU04198	AAY06959	AAY06942	AAW51095	AAB36189	AAU04199	AAW51089	AAB36183
	DB	20	19	21	22	20	20	19	21	22	19	21
	Query Match Length DB	280	280	280	280	288	256	276	276	276	280	280
æ	Query Match	100.0	94.2	94.2	94.2	93.2	85.4	85.4	85.4	85.4	85.4	85.4
	Score	103	46	26	46	96	88	88	88	88	88	88
	Result No.		7	e	4	2	9	7	8	6	10	11

Major antigenic pr E. chais P30-2 pro Ehrlichia canis im Ehrlichia chaffeen Ehrlichia chaffeen Variable surface a Ehrlichia canis im E. canis P30-1 pro E. canis P30-1 pro E. chaffeen E. chaffeen E. chaffeen E. chaffeen E. chaffeen E. chaffeen E. chaffeen Variable surface a Erlichia chaffeen Cowdria ruminantiu Cowdria ruminantiu Cowdria ruminantiu Cowdria ruminantiu Cowdria ruminantiu Major antigenic pr Variable surface a Ehrlichia canis pa Ehrlichia canis pa Ehrlichia canis pa Ehrlichia canis im	Arabidops Arabidops Arabidops Arabidops Arabidops C glutamic Senescence Melanogen	chafeensis; E. canis; P30;	chia chaffeensis and
AAU04193 AAY06962 AAY1479 AAX1479 AAX16196 AAX16196 AAX16964 AAX06964 AAY06964 AAY06964 AAY06964 AAX06964 AAX06947 AAX06947 AAX1093 AAX11478 AAX11478	AAG47084 AAG47111 AAG47110 AAG47110 AAG47109 AAG47109 AAC92136 AAC92136 AAY21976 AAX55866 AAK55866	280 AA. Ehrlichia c	s from Ehrlichia
280 22 281 22 281 22 281 22 286 20 2286 21 2286 21 2276 22 278 20 278 20 278 20 278 20 287 22 287 287 287 287 287 287 287 287 287 287	404000040	ein; ry) otein	98WO-US19600. 97US-0059353. IO STATE. hisa Y; 0/21. B. brane proteins f.
88 88 88 80 80 80 80 80 71 74 71 73 74 71 73 74 71 80 60 60 60 60 60 60 60 60 60 6	\$0.55 \$0.55 \$0.55 \$0.55 \$0.55 \$1.77 \$9.8	standard; 199 (first ensis OMP-1 ibrane prot i) dog.	3720-A1. R-1999. P-1998; P-1997;) UNIV OH i N, Rikii. 1999-254299 B: AAX3474 outer meml outer from can is 16; Fig 8:
11111111111111111111111111111111111111	0 6 6 6 4 4 4 4 4 4 4 6 6 6 6 6 6 6 6 6	Y06948 AAY06 AAY06 05-JU E. Ch Outer detec	XX XX PN W09913720 XX PD 25-MAR-19 XX XX PF 18-SEP-19 XX PR 19-SEP-19 XX XX OHIS) U XX

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          The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafebasis and E. canis. The E. chafebasis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in AAY06943-958. The E. canis proteins form part of the P30 family and consist of proteins form part of the P30 family and consist of proteins and genes are used to detect E. chafeensls in patients and E. canis in dogs.
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the full-length variable surface antigen VSA4 protein of Ehrlichia chaffeensis. Its amino acid sequence was deduced from a partial open reading frame (ORF4) of a genomic locus (see AAV07179) of E. chaffeensis that was obtained on the basis of homology to the major antigenic protein MAPI (see AAW18088) of Cowdria ruminantium. This genomic locus included 5 ORFs encoding similar, but non-identical proteins (see AAW19091-95). A claimed composition comprises a nucleic acid (see AAW1091-95). A claimed composition (see AAW51088-99) that elicits a protective immune response against rickettsial pathogen. The nucleic acid is used, in human or veterinary medicine, in vaccines to protect against Rickettsia, bhilichia, Anaplasma and Cowdria species. The Ehrlichia antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Composition containing nucleic acid encoding rickettsial antigen - useful for, e.g. stimulating protective immune response in humans or
                                                                                                                                                                                                  ó
                                                                                                                                                                    Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAP1 homologue; variable surface antigen; VSA4; rickettsia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McGuire TC;
                                                                                                                                                                                                    Indels
                                                                                                                                                                    Score 103; DB 20;
Pred. No. 5.9e-09;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1..25
/note= "putative signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mahan SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ganta RR,
                                                                                                                                                                                                                                                                                                                                        AAW51094 standard; Protein; 280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Ehrlichia chaffeensis VSA4 protein.
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                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                 1 NTTTGVFGLKQDWDGSTIS 19
                                                                                                                                                                                                                                                 97WO-US19044
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                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burridge MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barbet AF, Burridge MJ
Nyika A, Rurangirwa FR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ehrlichia chaffeensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYFL ) UNIV FLORIDA.
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N-PSDB; AAV07179.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                     14-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-APR-1998
                                                                                                                                                                                                                                                                                                                                                                         AAW51094;
                                                                                                                        Sequence
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animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
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AAW51094
ID AAW5
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The present sequence shows a high degree of similarity to the major antigonic protein 1 (MAP1) of Enritchia sp. The MAP1 gene may be used in a vaccines to protect animals or humans against rickettsial diseases caused by a organisms of Rickettsia sp., Ehrlichia sp., Anaplasma sp. or Cowdria sp. The vaccine elicits an immune response protective against the rickettsial pathogen. The nucleic acid vaccines can be driven by the human cytomegalovirus (HGWV) enhancer-promoter. Cowdria ruminatium genes designated map 2, Ihworf9, 4hworf1, 18hworf1 and 3gdorf3 may be used in therapeutic and diagnostic applications. The polypeptides are useful for detecting antibodies associated with infection by a rickettsial pathogen whilst the polynucleotides may be used to detect the presence of rickettsial nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides useful as DNA vaccines for conferring immunity to rickettsial infection e.g. heartwater caused by Cowdria ruminantium, comprises major antigenic protein 1 or 2 gene of rickettsial pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JC;
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 Ebrlichia chaffeensis; VSA4; variable surface antigen 4; MAP1; major antigenic protein 1; antirickettsial; vaccine; gene therapy; Rickettsia; Cowdria; Anaplasma; map2; lhworf3; 4hworf1; 18hworf1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SM, McGuire
Alleman AR;
                                                                                                                                     ;
polypeptides can be used diagnostically to detect antibodies associated with Ehrlichia infection (claimed).
                                                                                                Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 280;
                                                                                 Score 97; DB 19; Length zer
Pred. No. 5.7e-08;
Pred. Triches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ganta RR, Burridge MJ, Mahan
d AL, Simbi BH, Whitmire WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 97; DB 21;
Pred. No. 5.7e-08;
                                                                                                                                                                                                                                                                 AAB36188
ID AAB36188 standard; Protein; 280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 45-46; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    Ehrlichia chaffeensis partial VSA4.
                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barbet AF, Bowie MV, Ganta I
Rurangirwa FR, Moreland AL,
                                                                                              94.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-APR-2000; 2000WO-US10886.
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                                                                                                                                                                    NTTTGVFGLKQDWDGSTIS 19
                                                                                                                                                                                      99US-0130725
                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                Query Match
Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ehrlichia chaffeensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYFL ) UNIV FLORIDA.
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N-PSDB; AAC68705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                  280 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200065063-A2.
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                                                                                                                                                                                                                                                                                                                                                     02-MAR-2001
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                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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Matches

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The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in AAY06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAY06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30;
                                                                                                                                        Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            outer membrane proteins from Ehrlichia chaffeensis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 96; DB 20; Lv
Pred. No. 8.6e-08;
1; Mismatches 0;
 AAY06959 standard; Protein; 288 AA.
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Best Local Similarity 94.4%;
Matches 17; Conservative
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                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                        (OHIS ) UNIV OHIO STATE.
                                                                                                                                                                                                                                                                                                                                                                                                          Rikihisa Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ehrlichia chafeensis.
                                                                                                    E. canis P30 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-254290/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAX34759
                                                                                                                                                                                             Ehrlichia canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ehrlichia canis
                                                                                                                                                            detection; dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection; dog
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                                                                                                                                                                                                                             WO9913720-A1
                                                                                                                                                                                                                                                                                                                                   19-SEP-1997;
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                                                                                                                                                                                                                                                                                                   18-SEP-1998;
                                                                      05-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-1999
                                                                                                                                                                                                                                                                25-MAR-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                          Ohashi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY06942;
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   0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New MAP2 genes and polypeptides useful as vaccines for conferring immunity to human and animal rickettsial diseases, e.g. heartwater, or as molecular markers in nucleic acid analysis procedures
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   Gaps
                                                                                                                                                                                                                                                                                                 Major antigenic protein; MAP; vaccine; immunogenic; rickettsia; infection; heartwater; diagnostic; variable surface antigen; VSA.
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                                                                                                                                                                                                                                                              Variable surface antigen 4 (VSA4) from Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 97; DB 22; Length 280;
Pred. No. 5.7e-08;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nyika A;
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McGuire TC, Burridge MJ,
SM, Bowie MV, Alleman AR;
   ;
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Fig 2A-2B; 30pp; English
                                                                                                                                                       AAU04198 standard; Protein; 280 AA.
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94.78;
                                  97US-0953326
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                                                                                                                                                                                                                            23-OCT-2001 (first entry)
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Rurangirwa FR, Mahan SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 94.7
Matches 18; Conservative
   Conservative
                                                                                                                                                                                                                                                                                                                                                    Ehrlichia chaffeensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYFL ) UNIV FLORIDA
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N-PSDB; AAS07578.
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18;
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RESULT AAY06959

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Gaps

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Length 288; Indels

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Sequence
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AAB36189
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                                                                                                                                                                                                                                                    The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeneiss and E. canis. The E. chafecensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to 2) shown in AAVG643-95B. The E. canis proteins Grom part of the P30 family and consist of proteins shown in AAVG6559-970. The proteins and genes are used to detect E. chafeensis in patients and E. canis in dogs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tion containing nucleic acid encoding rickettsial antigenfor, e.g. stimulating protective immune response in humans or \ensuremath{\text{for}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                 Novel outer membrane proteins from Ehrlichia chaffeensis and
Ehrlichia canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAP1 homologue; variable surface antigen; VSA5; rickettsia;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 256;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 88; DB 20; Length 2:
Pred. No. 1.5e-06;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McGuire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ehrlichia chaffeensis VSA5 protein (partial sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "putative signal peptide'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1..25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW51095 standard; Protein; 276 AA.
                                                                                                                                                                                                                      Claim 18; Fig 1; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Fig 2B; 39pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                            85.4%;
84.2%;
97US-0059353.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-US19044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barbet AF, Burridge MJ,
Nyika A, Rurangirwa FR;
                                  (OHIS ) UNIV OHIO STATE.
                                                                      Ohashi N, Rikihisa Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYFL ) UNIV FLORIDA.
                                                                                                        WPI; 1999-254290/21.
N-PSDB; AAX34742.
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N-PSDB; AAV07179.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 16; Conser'
                                                                                                                                                                                                                                                                                                                                                                                      256 AA;
19-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW51095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Peptide
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This is the near full-length variable surface antigen VSA5 protein of Ehrlichia chaffeensis; it lacks about 5-7 cterminal amino acid residues. The VSA5 amino acid sequence was deduced from a partial open reading frame (ORF5) of a genomic locus (see AAV07179) of E. chaffeensis that was obtained on the basis of homology to the major antigenic protein MAPI (see AAM51088) of Cowdria ruminantium. This genomic locus included 5 ORFs encoding similar, but non-identical nucleic acid (see AAW51091-95). A claimed composition comprises a nucleic acid (see AAW51092) encoding a polypeptide (see AAW51088-99) pathogen. The nucleic acid is used, in human or veterinary medicine, in vaccines to protect against Rickettsia, Ehrlichia, Anaplasma and Cowdria species. The Ehrlichia antigenic polypeptides can be used diagnostically to detect antibodies associated with Ehrlichia infection (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides useful as DNA vaccines for conferring immunity to rickettsial infection e.g. heartwater caused by Cowdria ruminantium, comprises major antigenic protein 1 or 2 gene of rickettsial pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ganta RR, Burridge MJ, Mahan SM, McGuire TC; Id AL, Simbi BH, Whitmire WW, Alleman AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence shows a high degree of similarity to the major antigenic protein 1 (MAPI) of Ehrllichia sp. The MAPI gene may be used in a vaccines to protect animals or humans against rickettsial diseases caused by a organisms of Rickettsia sp., Ehrlichia sp.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ehrlichia chaffeensis; VSA5; variable surface antigen 5; MAP1; and inforestistis optotein 1; antirickettsial; vaccine; gene therapy; Rickettsia; Cowdria; Anaplasma; map2; Ihworf3; 4hworf1; 18hworf1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 88; DB 19; Le
Pred. No. 1.7e-06;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ehrlichia chaffeensis partial VSA5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 47; 63pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.4%;
84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-APR-2000; 2000WO-US10886.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NTTTGVFGLKQDWDGSTIS 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYFL ) UNIV FLORIDA.
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N-PSDB; AAC68706.
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Best Local Similarity
Matches 16; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rurangirwa FR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MO200065063-A2
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Sequence

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Anaplasma sp. or Cowdria sp. The vaccine elicits an immune response protective against the rickettsial pathogen. The nucleic acid vaccines can be driven by the human cytomegalovirus (HCMV) enhancer-promoter. Cowdria ruminatium genes designated map 2. Ihworf3, 4hworf1, 18hworf1 and 3gdorf3 may be used in therapeutic and diagnostic applications. The polypoptides are useful for detecting antibodies associated with infection by a rickettsial pathogen whist the polymucleotides may be used to detect the presence of rickettsial nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence represents the amino acid sequence of variable surface antigen 5 (VSA5) isolated from Ehrlichia chaffeensis, which has shimilarity to major antigen protein (MAP). The MAP polynucleotides and polypeptides are useful as vaccines for conferring immunity to rickettsia infection, including Cowdria ruminantium causing heartwater. The MAP polynucleotides may be used as molecular markers in nucleic acid analysis procedures, and to produce the MAP polypeptides, which may be used to raise antibodies that are reactive with the polypeptides. The nucleic acids may further be used as probes to identify complementary sequences within other nucleic acid molecules or genomes, where such probes can be applied to identify or distinguish infectious strains of organisms in diagnostic procedures or in rickettsial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New MAP2 genes and polypeptides useful as vaccines for conferring immunity to human and animal rickettsial diseases, e.g. heartwater, or as molecular markers in nucleic acid analysis procedures
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Major antigenic protein; MAP; vaccine; immunogenic; rickettsia; infection; heartwater; diagnostic; variable surface antigen; VSA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Variable surface antigen 5 (VSA5) from Ehrlichia chaffeensis.
                                                                                                                                                                                                                            ore 88; DB 21; Length 276;
ed. No. 1.7e-06;
Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nyika A;
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                                                                                                                                                                                                                              Score 88;
Pred. No. 1
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                                                                                                                                                                                                                              85.4%;
84.2%;
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                                                                                                                                                                                                                                                                                                     1 NTTTGVFGLKQDWDGSTIS 19
                                                                                                                                                                                                                                                                                                                         96US-0733230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-2001 (first entry)
                                                                                                                                                                                                                              Query Match
Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ehrlichia chaffeensis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYFL ) UNIV FLORIDA
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                                                                                                                                                                        276 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This polypeptide comprises the major antigen protein 1 gene (MAP1) of Ehrlichia chaffeensis. It is encoded by the MAP1 gene (see AAV07177). A claimed composition comprises a nucleic acid (see PANV07176-82) encoding a polypeptide (see AAW51088-99) that elicits a protective immune response against a rickettsial pathogen. The nucleic acid is used, in human or veterinary medicine, in vaccines to protect against Ricketsia, Ehrlichia, Anaplasma and Cowdria species. The nucleic acid does not replicate in the host but remains episomal and capable of expressing polypeptide for at least 19 mth. The Ehrlichia antigenic polypeptides can be used diagnostically to detect antibodies associated with Ehrlichia
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Composition containing nucleic acid encoding rickettsial antigen - useful for, e.g. stimulating protective immune response in humans or
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0
                                                                                                                                                                                                                                                                   MAP1 gene; major antigenic protein 1; rickettsia; DNA vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McGuire TC;
  Length 276;
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                           2; Indels
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                                                                                                                                                                                                                                        Ehrlichia chaffeensis major antigenic protein 1 (MAP1).
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84.2%; Pred. No. 1.7e-06;
ive 1; Mismatches 2;
Score 88; DB 22;
Pred. No. 1.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mahan SM,
                             Mismatches
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                                                                                                                                                     AAW51089 standard; Protein; 280 AA.
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 85.4%;
                                                                                                                                                                                                                                                                                                                                                                                  97WO-US19044.
                                                      1 NTTTGVFGLKQDWDGSTIS 19
                                                                                                                                                                                                                                                                                                                                                                                                            96US-0733230
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Best Local Similarity 84.2
Matches 16; Conservative
                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Burridge MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nyika A, Rurangirwa FR;
                                                                                                                                                                                                                                                                                              Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYFL ) UNIV FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infection (claimed).
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N-PSDB; AAV07177.
Query Match
Best Local Similarity
Matches 16; Conser
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The sequence represents the amino acid sequence of major antigenic protein! (MAPI) from Ehrlichia chaffeensis. The MAP polynucleotides and polypeptides are useful as vaccines for conferring immunity to rickettsia infection, including Cowdria ruminantium causing heartwater. The MAP polynucleotides may be used as molecular markers in nucleic acid analysis procedures, and to produce the MAP polypeptides, which may be used to raise antibodies that are reactive with the polypeptides. The nucleic acids may further be used as probes to identify complementary sequences within other nucleic acid molecules or genomes, where such probes can be applied to identify or distinguish infectious strains of organisms in diagnostic procedures or in rickettsial research where identification of particular organisms or strains is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New MAP2 genes and polypeptides useful as vaccines for conferring immunity to human and animal rickettsial diseases, e.g. heartwater, as molecular markers in nucleic acid analysis procedures
                                        Major antigenic protein 1; MAP1; vaccine; immunogenic; rickettsia; infection; heartwater; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30;
Major antigenic protein 1 (MAP1) from Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 85.4%; Score 88; DB 22; Length 28 Local Similarity 84.2%; Predci No. 1.7e-06. Indels es 16; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                        Barbet AF, Ganta RR, McGuire TC, Burridge MJ,
Rurangirwa FR, Mahan SM, Bowie MV, Alleman AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Column 15-17; 30pp; English.
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                                                                                                           Ehrlichia chaffeensis.
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                                                                                                                                                                                                                                                                                                                               (UYFL ) UNIV FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-424487/45.
N-PSDB; AAS07576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection; dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9913720-A1.
                                                                                                                                                    US6251872-B1
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                                                                                                                                                                                               26-JUN-2001.
                                                                                                                                                                                                                                                                                    17-0CT-1996;
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Best Local Si
Matches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY06943;
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                                                                                                                                                                                                               Ehrlichia chaffeensis; MAP1; major antigenic protein 1; antirickettsial; vaccine; gene therapy; Rickettsia; Cowdria; Anaplasma; map2; Ihworf3; 4hworf1; 18hworf1; 3gdorf3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotides useful as DNA vaccines for conferring immunity to rickettsial infection e.g. heartwater caused by Cowdria ruminantium, comprises major antigenic protein 1 or 2 gene of rickettsial pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barbet AF, Bowie MV, Ganta RR, Burridge MJ, Mahan SM, McGuire TC;
Rurangirwa FR, Moreland AL, Simbi BH, Whitmire WW, Alleman AR;
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Pred. No. 1.7e-06;
; Mismatches 2; Indels
                                      AAB36183 standard; Protein; 280 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                           21-APR-2000; 2000WO-US10886.
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Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                      Ehrlichia chaffeensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYFL ) UNIV FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-679675/66.
N-PSDB; AAC68700.
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                                                                                                                                                                                                                                                                                                                                                 WO200065063-A2:
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25-MAR-1999

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AAU04193

Length 280;

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The patent relates to homologous 28-kiloDalton (kDa) protein genes of Ehrlichia canis, designated ECa28SA1, ECa28SA2, ECa28SA3, ECa28-1 and ECa28-2. These genes are members of a polymorphic multiple gene family and contained in a single locus of 5.592 kb. The 28-kDa proteins are immunoreactive with anti-E. canis serum hence are important immunoprotective antigens. The protein is useful for vaccinating against E. canis infections such as canine ehrlichiosis in dogs. Canine ehrlichiosis, also known as canine tropical pancytopaenia, is a tick-borne rickettsial disease of dogs. ECa28-1 is conserved amongst different strains of E. canis and hence useful for serodiagnosis of canine ehrlichiosis. The present sequence is a E. canis ECa28SA3 30-kDa protein which is post-translationally modified to a
of the OMP family and consist of proteins OMP-1, -1(B to 2) shown in AAVO6943-95B. The E. canis proteins form part of the P30 family and consist of proteins shown in AAVO6959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homologous 28-kDa protein gene; ECa28SA3; immunoreactive; vaccine; p28 gene; p01% gene; po1,morphic multiple gene family; immunoprotective antigen; antibacterial; canine ehrlichiosis; canine tropical pancytopaenia; tick-borne rickettsial disease; serodiagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ehrlichia canis antigens useful for vaccinating against canine ehrlichiosis in dogs
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/label= Signal_peptide
24..280
/label= Mature_ECa28SA3_28-kDa_protein
                                                                                                                                                      77.7%; Score 80; DB 20; L. 73.7%; Pred. No. 3.5e-05; ive 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ehrlichia canis immunoreactive protein ECa28SA3.
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                                                                                                                                                                                                                                                                                                                                                                       AAY71479 standard; Protein; 280 AA.
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59 nstvgvfglkhdwnggtis 77
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Matches 14; Conservative
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                                                                                                   Sequence
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Peptide
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                                                                                                                                                                                                                                                                                                                               The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1. -1(8 Lo 2) shown in AAV06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAV06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                   Novel outer membrane proteins from Ehrlichia chaffeensis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 281;
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Pred. No. 1.7e-06;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY06962 standard; Protein; 280 AA.
                                                                                                                                                                                                                                                                                              Disclosure; Fig 3B; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85.4%;
                                                          97US-0059353
                    98WO-US19600
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Best Local Similarity 84.2.
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                                                                                                                                    Ohashi N, Rikihisa Y;
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N-PSDB; AAX34743.
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                    18-SEP-1998;
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AAY06962;

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AAY06962

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Sequence

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CC mature 28-kDa protein by cleavage of N-terminal signal sequence.
XX
SQ Sequence 280 AA:
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Sequence 280 AA;

0; Ouery Match 77.7%; Score 80; DB 21; Length 280; Best Local Similarity 73.7%; Pred. No. 3.5e-05; Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps

Db ò

Search completed: March 14, 2002, 09:09:38 Job time: 429 sec ,

Page 1

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

March 14, 2002, 09:24:53; Search time 32.82 Seconds (without alignments) 21.226 Million cell updates/sec Run on:

103 1 NTTTGVFGLKQDWDGSTIS 19 US-09-765-739A-7 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 segs, 36664827 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		фP			SUMMARIES		
Result No.	Score	Query Match	Length	DB	ID	Description	
г	51		540		YM8M_YEAST	26	
7	43.5		290	Н	AROE_SYNY3	P74591 synechocyst	
3	4		648		VP3_ВРР Н6	<u></u>	
4	42.5		734		PURL_ZYMMO		
5	41		135		FABE_BOVIN	,	
9	41		135		FABE_HUMAN	Q01469 homo sapien	
7	41		689		SYGB_PASMU	P57905 pasteurella	
8	41		866		YCBS_ECOLI		
6	40		115		GCSH_CHLPN	Q9z8b0 chlamydia p	
10	40	•	180		RBS_MARPA	marchantia	
11	40		282		BIOB_HELPJ		
12	40		282		BIOB_HELPY	025956 helicobacte	
13	40		377		YA67_METTH		
14	40		942		ENV_CAEVG	P31627 caprine art	
15	40		1025		DPYD_HUMAN	Q12882 homo sapien	
16	40		1191		NKC1_SQUAC		
17	39.5		366		GCST_NEIMB		
18	σ.		368		GCST_NEIMA		
19	39		282		PUNA_CELSP	P81989 cellulomona	
20	39		284		YQAK_BACSU	P45908 bacillus su	
21	39		285		SYGB_HAEAE		
22	39		307		YM16_MYCLE	_	
23	39		326		GBLP_NICPL	P93340 nicotiana p	
24	39		326		GBLP_TOBAC	nicotiana	
25	39		422		YF02_MYCPN	P75285 mycoplasma	
26	39		427		PYRC_BACCL		
27	39		428		YB01_MYCPN	P75568 mycoplasma	
28	39		438		YC05_MYCPN		
29	39		471		SYE_RHOSH		
30	39	37.9	473	Н	XYLA_CLOSR	P48790 clostridium	
31	39	37.9	688		SYGB_HAEIN	822	
32	39	37.9	756	-	K6PF_CAEEL	m	
33	39		896	-	POL_HTL1C	840	

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49.5%; Score 51; DB 1; 42.1%; Pred. No. 0.79; tive 3; Mismatches 8

Query Match
Best Local Similarity 42.15
Matches 8; Conservative

1 NTTTGVFGLKQDWDGSTIS 19

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Length 540;

P28774 artemia san Q2807 bos taurus Q2843 sus scrofa Q11069 caenorhabdi P0754 e pentafunc P2746 xiphophorus Q38362 mycobacteri P4813 cyanophora Q02278 mycobacteri P08186 escherichia P75302 mycoplasma O30207 archaeoglob		pdate) update) -CaT8 INTERGENIC REGION.	r's yeast). Saccharomycotina; Saccharomycetes; etaceae; Saccharomyces.	ndream M.A.; DDBJ databases. LIE PROFEIN (POTENT LITATOR FAMILY (ALL MILY). DHA12 SUBFA	yright. It is produced through a collaboration of Bioinformatics and the EMBL outstation. Institute. There are no restrictions on its tions as long as its content is in no way is not removed. Usage by and for commercial asprement (See http://www.isb-sib.ch/announce/isb-sib.ch).	Transmembrane.					ENTAL. 87D06CB0D70AF91 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BNBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLIZE=97061201; Deceloration of the property of the prope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PATHWAY: FOURTH STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY). SIMILARITY: BELONGS TO THE SHIKIMATE DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the enrise genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Length 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D90916; BAA18699.1; -.
InterPro; IPRO02907; Shikimate_DH.
Pfam; PFO4489; Shikimate_DH; 1.
Aromatic amino acid biosynthesis; Oxidoreductase; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 AA; 31099 MW; 8A2D38EE5D57B303 CRC64;
                                                                                                                                                                                                                                                                                                                                       Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; dsRNA viruses; Cystoviridae; Cystovirus.
NCBL_TaxID-10879;
                                                                                                                                                                       20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ARIMATES -DEHYDROGENASE (EC 1.1.1.25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 11, Created)
(Rel. 11, Last sequence update)
(Rel. 13, Last annotation update)
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                                                                                                                                              290 AA.
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SEQUENCE FROM N.A., AND SEQUENCE OF 1-13
                                                                                                                                                                                                                                                                                                             Synechocystis sp. (strain PCC 6803)
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256 NVPTNIHGLSMDWTGSALA 274
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Best Local Similarity 47.8
Matches 11; Conservative
                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteriophage phi-6
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SEQUENCE 290 AA
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P11129;
01-JUL-1989 (
01-JUL-1989 (
01-JAN-1990 (
P3_PROTEIN.
                                                                                                                                         AROE_SYNY3
P74591;
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AROE SYNY3
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MEDLINE-88160044; PubMed-3347997; Gottlibe P., Mergers. S., Romantschuk M., Carton J., Strassman J., Gottlibe P., Mergers S., Romantschuk M., Carton J., Strassman J., Bamford D.H., Kalkkinen N., Mindich L.; "Nucleotide sequence of the middle dsRNA segment of bacteriophage phi 6: placement of the genes of membrane-associated proteins."; Virology 163:183-190(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zymomonas mobilis.
Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  648 AA; 69178 MW; B188DFE02ACC54E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF213822; AAF23789.1; -.
InterPro; IPR000728; AIRS_related.
Pfan: PF00586; AIRS; 2.
Purine biosynthesis; Ligase; ATP-binding.
NP_BIND 106 117 ATP (POTENTIAL).
NP_BIND 106 177 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43; DB 1;
Pred. No. 20;
; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      734 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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734 AA; 77679 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M17462; AAA68485.1; -. PIR; C28648; P3BPF6. Envelope protein. SEQUENCE 648 AA: 69178 MW.
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us-09-765-739a-7.rsp

52 L -> P (IN REF. 1). 15074 MW; 439B86AF88A34E2A CRC64;

AA;

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52
135 A
                                                                                                                                                                                                                  FABE HUMAN
              SEQUENCE
CONFLICT
                                                                                                                                                                                                                                                                                                                   FABP5.
                                                                                                                                                                                    RESULT 6
FABE_HUMAN
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"Bovine epidermal fatty acid-binding protein: determination of ligand specificity and cellular localization in retina and testis.";

Blochemistry 37:3250-3257(1989)

"Bovine epidermal fatty acid-binding protein: determination of ligand specificity and cellular localization in retina and testis.";

"Blochemistry 37:3250-3257(1989)

"The Blochemistry 37:3250-3257(1989)

"THE UNSATURATED FATTY ACID PALMITATE (C16:0). MAY BE INVOLVED IN THE UPPARE AND TRANSORY OF FATTY ACIDS ESENTIAL FOR THE NOURISHMENT OF THE SURROUNDING CELL TYPES. IT IS A POTENTIAL TARGET FOR OXIDATIVE STRESS DURING CATARACT FORMATION IN LENS.

"SUBJECT OF THE SURFOUNDING CATARACT FORMATION IN LENS."

"ISSUE SPECIFICITY: MOST ABUNDANT IN LENS AND PRETINA (FOUND IN THE MUBLIER CELLS), MODERATELY ABUNDANT IN LENS AND TESTIS (FOUND IN THE SERTOLI CELLS), AND PRESENT IN VERY LOW AMOUNTS IN LUNG.

"THE SERTOLI CELLS), AND PRESENT IN VERY LOW AMOUNTS IN LUNG.

"THE SERTOLI CELLS), AND PRESENT IN VERY LOW AMOUNTS IN LUNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                Paworski C., Wistow G.;
'LP2, a differentiation-associated lipid-binding protein expressed in
                                                        Gaps
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                  FABE_BOVIN STANDARD; PRT; 135 AA.
P55052, 662808.
01-CCT-1996 (Rel. 34, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
A3-MAY-2000 (Rel. 39, Last annotation update)
ASSOCIATED LIPID BINDING PROTEIN, EPIDERMAL (E-FABP) (DIFFERENTIATION-ASSOCIATED LIPID BINDING PROTEIN LP2).
                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION (BY TYR-KINASES) (PROBABLE).
                            Length 734;
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 18-33 AND 116-129
                                                       5
                            DB 1;
                          Score 42.5; Di
Pred. No. 28;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00214; FABP; I.
Transport; Lipid-binding; Phosphorylation.
22 22 PHOSPHORYLATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P04117; 1ALB.
InterPro; IPR000463; Fatty_acid_BP.
InterPro; IPR000566; Lipocin_cytFABP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98198033; PubMed=9521644;
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97103094; PubMed=8947466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00061; lipocalin; 1. PRINTS; PR00178; FATTYACIDBP.
                          41.3%; 55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. J. 320:49-54(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF059507; AAC14711.1;
                                                                                                               551 TIGGVGLLQDWRDSTTIA 568
                                                                                   3 TIGVFGLKQDW-DGSTIS 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U55188; AAB41297.1;
                                                        Conservative
                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSPORTERS.
                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Retina;
                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Lens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            bovine lens.
                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Jaworski
                          Query Match
                                                                                                                                                        RESULT 5
FABE_BOVIN
                                                                                                                                                                                                                                                                                     FABP5
                                                       Matches
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                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIFFERENTIATION.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- TISSUE SPECIFICITY: KERATINOCYTES; HIGHLY EXPRESSED IN PSORIATIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PSORIASIS-ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Keratinocytes;
MEDLINE=92381332: PubMed=1512466;
Madsen P.S., Rasmussen H.H., Leffers H., Honore B., Celis J.E.;
Molecular cloning and expression of a novel keratinocyte protein
"Molecular sasociated fatty acid-binding protein (PA-FABP); that is
highly up-regulated in psoriatic skin and that shares similarity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Microsequences of 145 proteins recorded in the two-dimensional gel protein database of normal human epidermal keratinocytes."; Electrophoresis 13:960-969(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E., Vandekerckhove J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
   39.8%; Score 41; DB 1; Length 135, 47.6%; Pred. No. 7.8;
                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 67-72 AND 104-110, AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 25-33; 39-50; 62-71; 83-101 AND 120-129
                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PATTY ACID-BINDING PROTEIN, EPIDERMAL (E-FABE).
FATTY ACID-BINDING PROTEIN HOMOLOG) (PA-FABE).
                                                                                                                                                                                                                                                                                                                                                      135 AA
                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fatty acid-binding proteins.";
J. Invest. Dermatol. 99:299-305(1992).
                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Keratinocytes;
MEDLINE-93162043; PubMed-1286667;
                                                                                                                                                                  1 NTTTGVFGLKQDWDG--STIS 19
Query Match 39.89
Best Local Similarity 47.69
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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MAY B.J., Zhang Q., Li L.L., Pausitian M.L., Whittam T.S., Kapur V.;

"Complete genomic sequence of Pasteurella multocida Pm70.";

Proc. Natl. Acad. Sci. U.S.A. 98:4460-3465(2001).

"Complete genomic sequence of Pasteurella multocida Pm70.";

Proc. Natl. Acad. Sci. U.S.A. 98:4460-3465(2001).

"FROPHOSPHATE + L-GLYCYL-TRNA(GLY).

"STEDINGAPHATE + L-GLYCYL-TRNA(GLY).

"STELLARITY.

"STELLARITY
between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GLYCYL-TRNA SYNTHETASE BETA CHAIN (EC 6.1.1.14) (GLYCINE--TRNA LIGASE BETA CHAIN)
GLYS OR PM1102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE006151; AAK03186.1; -
InterPro; 1PR002311; tRNA_SML_2f. 1.
Pfam; PF02092; tRNA_SML_2f: 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patio on Fuzzos.
Pasteurial multocida.
Bacteria: Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.8%; Score 41; DB 1; Length 135; 47.6%; Pred. No. 7.8; tive 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                              InterPro; IPR000463; Fatty_acid_BP.
InterPro; IPR000565; Lipocln_cytFABP.
InterPro; IPR000565; Lipocalin. 1.
PRINTS; PR00178; FATTYACIDBP.
PROSTTE; PS00214; FABP; 1.
Transport; Lipid-Inding; 3D structure.
SEQUENCE 135 AA; 15164 MW; 77D38F8806143D63 CRC64;
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SEQUENCE 689 AA; 76019 MW; D67A980B5143B21E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          689 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=PM70;
MEDLINE=21145866; Pubmed=11248100;
                                                                                                                                                                                                                                                            Aarhus/Ghent-2DPAGE; 3007; IEF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 NTTTGVFGLKQDWDG--STIS 19
                                                                                                                                                                                                      EMBL; M94856; AAA58467.1; -. PDB; 1B56; 05-OCT-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pasteurella.
NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                           MIM; 605168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYGB_PASMU
P57905:
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RX MEDLINE-97061202; PubMed-8905232;

RX MEDLINE-97061202; PubMed-8905232;

RA OShima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,

RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,

RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,

RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,

RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,

RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,

RA Yano M., Horiuchi T.; 7-28 G. Min region on the linkage map.";

RY OFFICE CONTROL DE INVOLVED IN THE EXPORT AND ASSEMBLY OF THE PUTATIVE YCRO FIMBRIAL SUBMIT ACROSS THE OUTER MEMBRANE.

C. I- FUNCTION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE

C. SUBCELLUAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE

C. I- SIMILARITY: BELONGS TO THE FIMBRIAL EXPORT USHER FAMILY.

C. I- SIMILARITY: BELONGS TO THE FIMBRIAL EXPORT USHER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL OUTER MEMBRANE USHER PROTEIN
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SEXAIN=M.Z. / MGIGS5;
MEDILINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                           YCBS_ECOLI STANDARD; PRT; 866 AA.

YCBS_ECOLI STANDARD; PRT; 866 AA.

DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 40, Last annotation update)
DT 01-NOTHETICAL OUTER MEMBRANE USHER PROTEIN YCBS PRECURSOR.

GN YCBS OR B0940.

OS Escherichia coli.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS01151; FIMBRIAL_USHER; 1.
Hypothetical protein; Outer membrane; Fimbria; Transport; Signal; Complete proteome.
35 POTENTIAL.
  Score 41; DB 1; Length 689;
Pred. No. 46;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0004DC5E9F1F5796 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AE000196; AAC74026.1; -.
EMBL, D90732; BAA35695.1; -.
ECOGENE; EG13711; ycbs.
InterPro; IPR000015; Fimb_usher.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             866 AA; 95241 MW;
39.8%;
50.0%;
                                                                                                       :| ||:||: | || 459 DTLTGIFGIGQOPKGS 474
                      Similarity 50.0
8; Conservative
                                                                               1 NTTTGVFGLKQDWDGS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00577; Usher;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=562;
    Query Match
Best Local S
Matches 8
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Gaps

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Length 115; Indels

DB 1; 9.6;

38.8%; 57.1%;

Conservative

.. 8

19

Mismatches Score 40; Pred. No.

LIPOYL (BY SIMILARITY). 43FF43363A48D175 CRC64;

. 58 . 58 L 115 AA; 12876 MW;

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InterPro; IPR003016; Lipoyl.
Pfam; PF01597; GCV_H; 1.
PROSITE; PS00189; LIPOYL; FALSE_NEG.
  InterPro; IPR002930; GCV_H.
                                         Lipoyl; Complete proteome.
BINDING 58 58
                                                                                                                                                 6 VFGLKQDWDGSTIS
                                                                                                     Query Match
Best Local Similarity
                                                                    SEQUENCE
                                                                                                                            Matches
                                                                                                                                                                                                                    RBS_MARPA
  DR DR DR SO SO SO
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                                                                                                                                                                                                                                the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White C., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Elsen J., Fraser C.M.; Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY).

-1- SUBUNIT: THE GLYCINE CLEAVAGE SYSTEM IS COMPOSED OF FOUR PROTEINS:
P, T, L, AND H (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO THE GCVH FAMILY.

-1- SIMILARITY: CONTAINS 1 LIPOYL-BINDING DOMAIN.
                        Gaps
                                                                                                                                                                                                                                                                                     Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative grammoos of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).
                        ;
  DB 1; Length 866;
                                                                                                                                                                                           GCVH OR GCSH OR CPN0433 OR CP0320.
Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
                        3;
                                                                                                                            115 AA.
                                                                                                                                                          20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update PROBABLE GLYCINE CLEAVAGE SYSTEM H PROTEIN.
                       1; Mismatches
  Score 41;
             Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic Acids Res. 28:1397-1406(2000).
                                                                                                                                                                                                                                                                         MEDLINE-99206606; PubMed-10192388;
                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20150255; PubMed=10684935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AE001626; AAD18577.1; -. EMBL; AE002194; AAF38175.1; -. EMBL; AP002546; BAA98641.1; -. HSSP; P16048; 1HTP.
                                                                                                                                               20-AUG-2001 (Rel. 40, Created)
39.8%;
63.6%;
                       Conservative
                                                                                                                           STANDARD;
                                                                  723 GLKTDWRGYTV 733
                                           8 GLKQDWDGSTI 18
           Local Similarity
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                             NCBI_TaxID=83558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P16048; 11
TIGR; CP0320; -
                                                                                                                                                                                                                                                                STRAIN=CWL029
                                                                                                                                                                                                                                                                                                                                                        STRAIN=AR39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=J138
                                                                                                                          GCSH_CHLPN
 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between
                                                                                                                                     Q9Z8B0;
                                                                                                              GCSH_CHLPN
                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marchantia paleacea.
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Marchantiophyta;
Marchantiales; Marchantiaceae; Marchantia.
NCBI_TaxID=56867;
                                                                                                                                                                                                                                                                                      15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN, CHLOROPLAST PRECURSOR (EC 4.1.1.39) (RUBISCO SMALL SUBUNIT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probom; PD000290; RuBisCo_small; 1.
Photosynthesis; Carbon dioxide fixation; Photorespiration;
Lyases, Oxidoreductase; Monooxygenase; Chloroplast; Transit peptide.

1 58 CHLOROPLAST (BY SIMILARITY).
CHLOROPLAST (BY SIMILARITY).
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE CARBOXYLATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-VAR. DIPTERA; TISSUE-Callus;
BUDLINE-92025705; PubMed-10189707.
Suzuki T., Takio S., Tanaka K., Yamamoto I., Satch T.;
"Differential light regulation of the rbcS gene expression in two call lines of the liverwort Marchantia paleacea var. diptera.";
Plant Cell Physiol. 40:100-103(1999).
-i- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) = 3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.
-i- SUBUNIT: B LARGE CHAINS + 8 SMALL CHAINS.
-i- SUBCELLULAR LOCATION: CHLOROPLAST.
-i- SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) 2 3-PHOSPHO-D-GLYCERATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D736A467732CDCB4 CRC64;
                                                                                                                                                                                                                     AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB004883; BAA28610.1; -. InterPro; IPR000894; RuBisCO_small.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00101; RuBisCO_small; 1
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                                                                                                                                                                                                                STANDARD;
97 VVRLDQDWDPSNLS 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTIVE SITE
                                                                                                                                                                                                            RBS_MARPA
064416;
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STRAIN—26695 / ATCC 700392;
A STRAIN—26695 / ATCC 700392;
A Tomb J. F. White O. Kerlavage A.R. Clayton R.A., Sutton G.G.,
A Floatschmann R.D. Ketchum K.A., Klenk H.-P. Gill S., Dougherty B.A.,
A Loftus B., Richardson D. Dodson R., Khalak H.G., Glodek A.
A McKenney K., Fitzgerald L.M., Fulli C., Glodek B.R.,
A Cotton M.D., Weidman J.M., Fulli C., Bowman C., Watthey E.K.,
A Cotton M.D., Weidman J.M., Fulli C., Bowman C., Watthey L.,
A Venter J.C., Watthey D.D., Cotton M.D., Kelley J.M.,
A Venter J.C., Mark P.D., Smith H.O., Fraser C.M.,
The complete genome sequence of the gastric pathogen Helicobacter
C. CARATYTIC ACTIVITY: DETHIOBIOTIN + (S) = BIOTIN.
C. I CARATYTIC ACTIVITY: DETHIOBIOTIN + (S) = BIOTIN.
C. SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation use by non-profit institutions as long as its content is not modified and this statement is not removed. Usage by and for commercial or send an email to license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori (Campylobacter pylori).
Bacteria, proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter.
NCBL_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-DELTA H;
MEDLINE=98037514; PubMed-9371463;
Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MTH1067. WHO METHOD WAS A METHOD WAS A METHOD WE WELL WAS A METHOD WAS A METH
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Pred. No. 25;
3; Mismatches 2; Indels
                                                     SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
YA67_METTH

TA YA67_METTH

AC 027139;
TI 5-U10-1998 (Rel. 36, Last sequence update)
DT 15-U10-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DT 30-AUG-2001 (Rel. 40, Last annotation update)
DS METHBIOGT (Rel. 40, Last annotation update)
CS Methanocacterium thermoautotrophicum.
CC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriales; Methanothermobacter.
CX NCB: TAZIN-145.262;
RN SEQUENCE FROM N.A.
RS SEQUENCE FROM N.A.
R MEDLINE-98037514, PubMed-9371463;
RA MEDLINE-98037514, PubMed-9371463;
RA SELINE-98037514, Pubmed-9371463;
RA SELINE-SEGIAN N.A.
RA MEDLINE-SEGIANM TA SEGIANM TA SEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match
Local Similarity 50.0%;
es 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 GIFGLNESWE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 GVFGLKQDWD 14
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Matches
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                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALM R.A. LING L.-S.L., MOIR D.T., KING B.L., Brown E.D., Doig P.C., Alm R.A. Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C., Smith D.R., Noonan B., Gulld B.C., deJonge B.L., Carmel G., Glbson R., Merberg D., Mills S.D., Jiang O., Taylor D.E., Vovis C., "Genomic sequence comparison of two unrelated isolates of the human sy: 176-18(1999).

- CAPALYTIC ACTIVITY: DETHIOBIOTIN + (S) = BIOTIN.
- PATHARY: LAST STEP IN BIOTIN BIOSYNTHESIS PATHWAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria: Proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter.
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                                                                                                                 9
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EMBL; AEO01553. AAD06676.1;

EMBL; AEO01553. AAD06676.1;

InterPro; IPR002684; Blotin_synth, 1.

Biotin blosynthesis; Iron-sulfur; Transferase; Complete proteome. 17

METAL 17 11 IRON-SULFUR (POTENTIAL).

METAL 21 IRON-SULFUR (POTENTIAL).

14 24 11 IRON-SULFUR (POTENTIAL).

1400 MW; 3A07177B65AFAFIB CRC64;
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                              38.8%; Score 40; DB 1; Length 180;
42.9%; Pred. No. 16;
tive 3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                         20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last Sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
BIOTHN SYMTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE).
                                                                                                                                                                                                                                                                                                                                           282 AA.
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15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
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Pred. No.
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                                                                                                                               5 GVFGLKQDW-----DGSTIS 19
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Best Local Similarity 50.0%;
Matches 5; Conservative
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Query Match
Best Local Similarity
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Q9ZJK8;
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BIOB_HELPY
ID BIOB_HELPY
AC 025956;
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BIOB_HELPJ

DD HODE_H

AC 092JKB

DT 20-AUG

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DT 20-AUG

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DPYD_HUMAN
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                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Juwani N., Caruso, A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics."; J. Bacteriol. 179:7135-7155(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structure and genetic variability of envelope glycoproteins of two antigenic variants of caprine arthritis-encephalitis lentivirus."; J. Virol. 65:5744-5750(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
RSOR (COAT POLYPROTEIN) [CONTAINS: SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND SEQUENCE OF 81-95.
MEDLINES-92015464; PubMed=1656067;
Knowles D.P. Jr., Cheevers W.P., McGuire T.C., Brassfield A.L.,
Harwood W.G., Stem T.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                       Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caprine arthritis encephalitis virus (strain G63) (CAEV).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11662;
                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
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                                                                                                                                                                                                                                                                                                                      InterPro; IPR000531; TonB_boxC.
Hypothetical protein; Complete proteome.
SEQUENCE 377 AA; 42021 MW; 24C0EE1FA77C7AE4 CRC64;
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Pred. No. 35;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         942 AA.
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20-AUG-2001 (Rel. 40, Last sequ
20-AUG-2001 (Rel. 40, Last anno
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PIR; A41307; VCLJC6.
IntherPro: IPRO0238; Env_GP41.
Pfam: PF00517; GP41; 1.
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Best Local Similarity 35.7
Matches 5; Conservative
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Gaps
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012882; Q16694; Q16761;
01-NOV-1997 (Rel. 35, Created)
101-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DIHYDROPYRIMIDINE DEHYDROGENASE (NADP+) PRECURSOR (EC 1.3.1.2) (DPD) (DHPDRASE) (DIHYDROURACIL DEHYDROGENASE) (DIHYDROTHYMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "CDNA cloning and chromosome mapping of human dihydropyrimidine dehydrogenase, an enzyme associated with 5-fluorouracil toxicity and congenital thymine uraciluria.";
J. Biol. Chem. 269:23192-23196(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-94365020; PubMed-8083224;
Yokota H., Fernandez-Salguero P., Furuya H., Lin K., McBride O.W.,
Podschun B., Schnackerz K.D., Gonzalez F.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                      SURFACE PROTEIN (POTENTIAL).
TRANSMEMBRANE PROTEIN (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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Johnson M.R., Wang K., Tillmanns S., Albin N., Diasio R.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 942; 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 5B0E1F0F3D355F4A CRC64;
Polyprotein; Transmembrane.
                                                                                                       EXTRACELLULAR (POTENTIAL)
                                                                          CYTOPLASMIC (POTENTIAL). POTENTIAL).
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Pred. No.
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46.2%;
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482 NTITGIMGTNTNW 494
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - SUBUNIT HOMODIMER.
- SUBUNIT HOMODIMER.
- SUBUNITH HOMODIMER.
- SUBUNITH HOMODIMER.
- SUBUNITH HOMODIMER.
- SUBUNITH HOMODIMER.
- SUBCELLULAR LOCATION: CYTOPLASMIC.
- SUBCELLULAR LOCATION: CYTOPLASMIC.
- DISEASE: DEPECTS IN DEVE ARE THE CAUSE OF HEREDITARY THYMINE-
URACILURIA (ALSO KNOWN AS FAMILIAL PYRIMIDINEMIA), A DISEASE
CHARACTERIZED BY PERSISTENT URINARY EXCRESION OF EXCESSIVE AMOUNTS
OF URACIL, THYMINE AND S-HYDROXYMETHYLURACIL. PATIENTS SUPFERING
FROM THIS DISEASE SHOW A SEVERE REACTION TO THE ANTICANCER DRUG S-
FLUOROURGACIL. THIS REACTION INCLUDES STOMATITS, LEUKOPENIA,
THROMBOCYTOPENIA, HAIR LOSS, DIRARHEA, FEVER, MARKED WEIGHT LOSS,
CEREBELLAR ATAXIA, AND NEUROLOGIC SYMPTOMS, PROGRESSING TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lu Z.-H., Zhang R., Diasio R.B., "Purification and characterization of dihydropyrimidine dehydrogenase
"Structural organization of the human dihydropyrimidine dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS ARG-29; TRP-235 AND HIS-886.
MEDLINE-97411371; PubMed-9266349;
VECKER P., van Kuilenburg A.B.P., Meinsma R., van Gennip A.H.;
"Identification of novel point mutations in the dihydropyrimidine
                                                                            TISSUE=Liver;

MEDLINE=97047101; PubMed-8892022;
Vreken P., Van Kuilenburg A.B.P., Meinsma R., Smit G.P.A.,

Bakker H.D., de Abreu R.A., Van Gennip A.H.;

A point mutation in an invariant splice donor site leads to exc

skipping in two unrelated Dutch patients with dihydropyrimidine
                                                                                                                                                                      dehydrogenase deficiency.";
J. Inherit. Metab. Dis. 19:645-654(1996).
                                                                                                                                                                                                                      CHARACTERIZATION, AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                 from human liver.";
J. Biol. Chem. 267:17102-17109(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM: 274270;
InterPro; IPR001450; 4FE4S_ferrdxin.
InterPro; IPR001295; DHO_dh.
                                                                                                                                                                                                                                  TISSUE=Liver;
MEDLINE=92381021; PubMed=1512248;
                                Cancer Res. 57:1660-1663(1997).
                                                              581-635 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U09178; AAA57474.1; -. EBBL; U20938; AAB51366.1; -. EMBL; X95670; CAA64973.1; -. HSSP; P26886; IERD.
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                                                              SEQUENCE OF
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IRON-SULEUR 1 (FEE-4S) (POTENTIAL).
IRON-SULEUR 1 (FEE-4S) (POTENTIAL).
IRON-SULEUR 1 (FEE-4S) (POTENTIAL).
IRON-SULEUR 1 (FEE-4S) (POTENTIAL).
IRON-SULEUR 2 (FEE-4S) (POTENTIAL).
C-> R (IN DPYD*9A AND DPYD*9B; LOSS OF
                                                                             DIHYDROPYRIMIDINE DEHYDROGENASE [NADP+].
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                   /FIG=VAR_005173.

R -> W (IN PPEPB*8). LOSS OF ACTIVITY).

FTIG=VAR_005174.

S -> N (IN DPEPB*4). LOW ACTIVITY).

FTIG=VAR_005175.

I -> V (IN DPEPB*5).

/FTIG=VAR_005176.

FTIG=VAR_005177.

V -> F (IN DPEPB*8). LOW ACTIVITY).

V -> F (IN DPEPB*8).

FTIG=VAR_005177.

V -> F (IN DPEPB*10). LOW ACTIVITY).

FTIG=VAR_005177.

V -> F (IN DPEPB*10). LOW ACTIVITY).

S -> N (IN REF. 2).

S -> N (IN REF. 2).
InterPro; IPR003009; FMN_enzyme.
Pfam; FF01180; D40dehase; 1.
Pfam; F000137; Fer4; 2.
PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
Oxidoreductase; NADP; Flavoprotein; FAD; FMN; Iron-sulfur; 4Fe-4S; Disease mutation.
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                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 1; Length 1025;
Pred. No. 1e+02;
2; Mismatches 3; Indels
                                                                                                                URACIL-BINDING (POTENTIAL)
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Job time: 909 sec
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58.3%;
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1025 AA;
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(without alignments)
25.409 Million cell updates/sec
                                                                                                               March 14, 2002, 09:10:46; Search time 56.96 Seconds
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                219241 seqs, 76174552 residues
                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                               103
1 NTTTGVFGLKQDWDGSTIS 19
                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                             US-09-765-739A-7
                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                   Perfect score:
                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                     Run on:
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Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_68:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	surface	surface	surface	28k surface antige	major antigenic pr	28k surface antige		RIX	flagellin - Escher	aminoacyl-histidin	hypothetical prote		hypothetical prote	C		al		hypothetical prote	Ø	hypothetical prote	•~			u	_	probable outer mem	\sim		hypothetical prote
SUMMARIES	QI	JE0217	JE0218	JE0219	JE0216	I40882	JE0221	S54586	B85547	C48658	C82096	C86822	C83242	S76787	A75466	S63457	G85354	P3BPF6	T40502	A84110	S34346	156326	F75255	E84885	B82220	F85620	183	A96682	775	T27307
	DB	7	ď	~	7	7	7	7	7	7	7	7	N	7	7	~	7	Н	7	7	7	7	7	7	7	7	7	7	~	7
	Length	280	276	286	278	284	133	540	5188	584	534	1649	267	290	160	185	490	648	384	293	118	135	185	244	335	653	998	1055	വ	82
de	Query	94.2	85.4	Н	58.3	57.3	Э.	49.5		45.6	42.7	42.7	42.2	42.2		41.7	41.7	41.7	40.8	•		9.	ģ.	•	39.8	•	9	39.3		38.8
	Score	97	88	74	9	29	55	51	49	47	44	44	٠	43.5	43	43	43	43	42	41.5	41	41	41	41	41	41	41	40.5	40.5	40
	Result No.		7	9	4	S	ø	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

	ALIGNMENTS					
procein-tylosine-p	A49724	-	1118	38.8	40	45
dihydropyrimidine	A54718	7	1025	38.8	40	44
env polyprotein pr	VCLJC6	-	964	38.8	40	43
penicillin-binding	A83800	7	719	38.8	40	42
hypothetical prote	F85809	7	582	38.8	40	41
probable leucyl am	G75483	~	482	38.8	40	40
tetracycline 6-hyd	JC4098	7	470	38.8	40	39
hypothetical prote	S76830	7	408	38.8	40	38
probable phosphoes	877505	7	404	38.8	40	37
acetyltransferase	F69008	7	377	38.8	40	36
probable membrane	T36845	7	319	38.8	40	35
hypothetical prote	T23932	7	299	38.8	40	34
biotin synthetase	H71823	7	282	38.8	40	33
biotin synthetase	F64695	7	282	38.8	40	32
glycine cleavage s	C72079	~	115	38.8	40	31
glycine cleavage s	G86544	~	115	38.8	40	30
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RESULT 1 JEGOTA	ä
99 Allem y of	
ar-19 .J.; famil	Gaps
17-м gene	0)
nange ırridi igen g	280; els
ext_cl M.; Bu	ength Ind
98 #t. n, S.i 8 urfac	2; L -08; 1;
s ug-19 Maha , 199 kDa s	DB 5.5e ches
fensi 21-A 21-A A.F.; 6-643 a 28	Score 97; DB 2; Length 280 Pred. No. 5.5e-08; 0; Mismatches 1; Indels
chaf ision bet, 7, 63 on of 98321	Scor Pred 0; M
ichia isis 'e_rev ', Bar in. 24 ilzati MUID:	94 2%; Score 97; DB 2; Length 280; 94.7%; Pred. No. 5.5e-08;
Ehrl adfen squenc C.R. Commusacter)216;	94 , 94 :vativ
en 4 · · · · · · · · · · · · · · · · · ·	larit; Conse
antige names hr1icl ug-19 JE02; Su, Su, Su, Phys. ecula: numbe: JE02 JE02	h Simi 18;
RESULT 1 JEOUR 1 JEOUR 1 JEOUR 20 JEOUR 30 JEOUR	Query Match Best Local Similarity 94.7%; Matches 18; Conservative C
RESULT JE0217 28k sur V) Alter C; Speci C; Date: C; Acces R; Refer A; Title A; Title A; Molec A; Resid A; Coss	Query Best Match
A A A A A A A A A A A A A A A A A A A	

9 RESULT δ g

Species: Ehrlichia chaffensis
N:Alternate names: MAPI
C;Species: Ehrlichia chaffensis
C;Species: Ehrlichia chaffensis
C;Species: Ehrlichia chaffensis
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1999 #text_change 17-Mar-1999
C;Accession: JE0218
R;Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R. Bacchem. Blophys. Res. Commun. 247, 636-643, 1998
A;Title: Molecular characterization of a 28kDa surface antigen gene family of the tri
A;Reference number: JE0218
A;Accession: JE0218
A;Accession: JE0218
A;Molecule type: DNA
A;Residues: 1-276 <RED>A;Cross-references: GB:AF062761 ö Gaps ö 85.4%; Score 88; DB 2; Length 276; 84.2%; Pred. No. 1.5e-06; iive 1; Mismatches 2; Indels Query Match 85.4 Best Local Similarity 84.2 Matches 16; Conservative

1 NTTTGVFGLKQDWDGSTIS 19 δλ Dρ

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Gaps

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Probable
C; Species: Saccharomyces cerevisiae
C; Cpate: 08-Jul-1995 #sequence_revisiae
C; Cpate: 08-Jul-1995 #sequence_revisiae
C; Cpate: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 05-Nov-1999
R; Pearson, D; Bowman, S
Submitted to the EMBL Data Library, May 1995
A; Reference number: S3458
A; Reference number: S3458
A; Residues: 1-540 < Peps.
A; Residues: 1-540 < Peps.
A; Residues: 1-540 < Peps.
A; Coss references: EMBL:249704; NID:9825540; PIDN:CAA89777.1; PID:9825545; GSPDB:GNO
A; Genetics:
A; Map Pooition: 13R
C; Seperimental source: strain AB972
C; Genetics:
C; Cogentics:
C; Cogentics:
C; Cogentics:
C; Stoperiamily: aminorriazole resistance prodicted <TM2>
C; Stoperiamily: mainorriazole resistance predicted <TM2>
F; 139-155, Toomain: transmembrane #status predicted <TM3>
F; 268-249 / Domain: transmembrane #status predicted <TM5>
F; 281-249 / Domain: transmembrane #status predicted <TM5>
F; 281-249 / Domain: transmembrane #status predicted <TM5>
F; 281-249 / Domain: transmembrane #status predicted <TM5>
F; 381-351 / Domain: transmembrane #status predicted <TM6>
F; 381-381 / Domain: transmembrane #status predicted <TM6>
F; 381-381 / Domain: transmembrane #status predicted <TM6>
F; 381-381 / Domain: transmembrane #status predicted <TM
                                                                                                                                                                                                                                                                                                                                            28k surface antigen 2 - Ehrlichia canis
C;Species: Bhrischia canis
C;Species: Ehrlichia canis
C;Species: Dray1998 #sequence_revision 21-Aug-1998 #text_change 21-Jul-2000
B;Chacession: JEG221
B;Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.
A;Title: Molecular characterization of a 28kDa surface antigen gene family of the tr
A;Arcession. JEG221
A;Accession. JEG221
A;Molecule type: DNA
A;Residues: 1-133 <a href="Molecular characterization">Molecular characterization of a 28kDa surface antigen gene family of the tr
A;Accession. JEG221
A;Accession. JEG221
A;Cross.references: GB:AF062762; NID:g3327964; PIDN:AAC26722.1; PID:g3327966
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                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 51; DB 2; Length 540;
Pred. No. 2.5;
3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Indels
                                                                           5,
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Pred. No. 0.12;
3; Mismatches
                                                               Mismatches
                                                      1;
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Conservative 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sucify match
Best Local Similarity 58.8%;
Matches 10; Conservative
                     Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 TTGVFGLKODWDGSTIS 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 TTVVYGLKENWAGDAIS 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | : || || || ::
256 NVPTNIHGLSMDWTGSALA 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NTTTGVFGLKQDWDGSTIS 19
                                                                                                3 TTGVFGLKQDWDG 15
                                                                                                                                                   63 TKAVFGLKKDWDG
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Best Local Similarity
Trahes 8; Conserve
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28k surface antigen 2 - Ehrlichia chaffensis
28k surface antigen 2 - Ehrlichia chaffensis
NAlternate names: MAPI
C; Species: Ehrlichia chaffensis
C; Species: Ehrlichia chaffensis
C; Accession: JE0219
Biochem. JE0219
Biochem. Biophys. Res. Commun. 247, 636-643, 1998
A; Reddy G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
A; Rederence number: JE0216; MUID:98321180
A; Reference number: JE0216; MUID:98321180
A; Recession: JE0219
A; Residues: 1-286 < RED>
A; Residues: 1-286 < RED>
A; Residues: 1-286 < RED>
A; Residues: JE080
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28k surface antigen 3 - Ehrlichia chaffensis

N'Alternate names: MAPI

C'Species: Ehrlichia chaffensis

C'Species: D'Species: English (Errichia)

Biochem. JE0216

Biochem. Biophys. Res. Commun. 247, 636-643, 1998

A'Accession: JE0216

A'Accessi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  major antigenic protein - heartwater rickettsia
C;Species: Cowdria ruminantium (heartwater rickettsia)
C;Date: 16-Way-1996 #sequence_revision 16-Mag-1996 #text_change 08-Oct-1999
C;Accession: 140882; 842827
R;Van Vilet, A.H. Jongejan, F.; van Kleef, M.; van der Zeijst, B.A.
A;Title: Molecular cloning, sequence analysis, and expression of the gene encoding the A;Title: Molecular cloning, sequence analysis, and expression of the gene encoding the A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-284 <RES>
A;Cross-references: EMBL:X74250; NID:g454266; PIDN:CAA52309.1; PID:g454267
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.8%; Score 74; DB 2; Length 286
68.4%; Pred. No. 0.00026;
Live 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 278; 0.044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 59; DB 2;
Pred. No. 0.065;
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52.6%; Pred. No. 0.04
tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NTTTGVFGLKQDWDGSTIS 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 68.4:
Matches 13; Conservative
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Best Local Similarity 52.6
Matches 10; Conservative
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Best Local Similarity
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Gaps

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C. Species: Pseudomonas aeruginosa
C. Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C. A. Scover, C. K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lory, S.; Olson, M.V.
Nature: 406, 959-964, 2000
A. Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A; Reference number: A82950; MUID: 20437337
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-267 <STO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein yqbK [imported] - Lactococcus lactis subsp. lactis (strain IL140 C.Specias: Lactococcus lactis subsp. lactis (c) specias: Lactococcus lactis subsp. lactis (c) specias: Lactococcus lactis subsp. lactis (c) bate: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001 E.Specias: Lactococcus lactis was considered. P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Eh Genome Res. in press, 2001
A; Reference number: A86625
A; Reference number: A86625
A; Reference number: A86625
A; Reterence number: A86625
A; Reterence number: A86625
A; Reference nu
                 A)Cross-references: GB:AE004299; GB:AE003852; NID:99656835; PIDN:AAF95423.1; GSPDB:GN A)Experimental source: serogroup O1; strain N16961; biotype El Tor C,Genetics: A;Gene: VC2279 A;Map,position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GB:AE004091; NID:99949350; PIDN:AAG06627.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-1649 <STO>
A;Cross-references: GB:AE005176; NID:g12724583; PIDN:AAK05677.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 267;
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                                                                                                                                                                                                                                                                             Length 534;
                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44; DB 2; I
Pred. No. 1.1e+02;
I; Mismatches 4;
                                                                                                                                                                                                                                                                             2;
                                                                                                                                                                                                                                                                         Score 44; DB 2
Pred. No. 32;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43.5; DB
Pred. No. 18;
1; Mismatches
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                                                                                                                                                                                                                                                                         42.7%;
70.0%;
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larity 46.7%;
Conservative
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Best Local Similarity 58.8
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             198 TGAFGLKEGW 207
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Best Local Similarity
Matches 7; Conserv
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                              4 TGVFGLKQDW 13
A; Residues: 1-534 <HEI>
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                                                  probable RTX family exoprotein [imported] - Escherichia coli (strain 0157:H7)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C;Accession: B85547
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-5188 <STO>
A;Residues: 1-5188 <STO>
A;Cesidues: 1-5188 <STO>
A;Cesidues: 1-5188 <STOA
A;Cesidues: 1-5188 <STOA
A;Cesidues: 1-5188 <STOA
C;Cenetics:
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Cispecies: Escherichia coli
Cispecies: Escherichia coli
Cispecies: Scherichia coli
Cispecies: Scherichia coli
Cispecies: Careasion: C48658
Ciscorentale, G.; Whitfield, C.
J. Bacteriol. 175, 5395-5402, 1993
A;Title: Comparative analysis of flagellin sequences from Escherichia coli strains posse
A;Reference number: A48658; MUID:93374833
A;Accession: C48658
A;Accession: C48658
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-584 <SCH>
A;Residues: 1-584 <SCH>
A;Cross-references: GB:L07388; NID:9290438; PIDN:AAA23798.1; PID:9290439
C;Superfamily: flagellin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: C82096
R;Heidelberg J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, B. R. R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
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A;Accession: C82096
A;Status: preliminary
A;Molecule type: DNA
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Pred. No. 12;
3; Mismatches
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Pred. No.
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66.78;
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4803 TTSGVAAMDYDWDGA 4817
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199 NTTTGLYGLKTE 210
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Best Local Similarity
Matches 8; Conserv
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Matches 8; Conserv
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C:Species: Saccharomyces cerevisiae
C:Accession: S63457
R:Wang, Y: Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Hall, J.; Storms, R.K R:Wang, Y: Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Hall, J.; Storms, R.K A; Reference number: S63457
A; Accession: S63457
A; Residues: 1-185 cWans
A; Residues: 1-185 cWans
A; Residues: 1-185 cWans
A; Residues: 1-185 cWans
A; Cenetics: EMBL:U36624; NID:g1276642; PID:g1039452; GSPDB:GN00016; MIPS:YPLC
A; Map position: 16L
C; Superfamily: Saccharomyces hypothetical protein YPL025c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 52.6%; Pred. No. 15;
Matches 10; Conservative 1; Mismatches 2; Indels
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Synchotter 13
Synchotter 2576787
Synchotter 25-Apr-1997
Synchotter 25-Apr-1996
Synchotter 25-Apr-1997
Sy
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A; Reference number: S76787
A; Accession: S76787
A; Molecule type: DNA
A; Status: 1-290 < KANA.
A; Cross-references: EMBL: D90916; GB: AB001339; NID:g1653715; PIDN:BAA18699.1; PID:g165378
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996; Superfamily: shikimate dehydrogenase; shikimate dehydrogenase homology <SKD>
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C.Species: Deinococcus radiodurans
C.Saccession: A7346
E.Accession: A7346
E.White, O.: Elsen, J.A.; Hedelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
F.White, O.: Elsen, J.A.; Hedelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
Science 286, 1571-1577, 1999
A.Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R.J.
A.Accession: A7546
A.Status: preliminary
A.Science 286, MUID:20036896
A.Status: preliminary
A.Status: Terliminary
A.Status: L.J. O-CHILL
A.STATUS: L.J. O-CH
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Pred. No. 13;
3; Mismatches 4; Indels
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145 NTTFGVLGL---WDPAT 158
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50.08;
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A;Experimental source: strain R1
C;Genetics:
A;Gene: DR0859
A:Map position: 1
C;Keywords: methyltransferase
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Best Local Similarity 50.00
Matches 7: Conservative
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RESULT 15 86345. hypothetical protein YPL025c - yeast (Saccharomyces cerevisiae) N;Alternate names: hypothetical protein LPB6c Qγ qq

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Sequence 4, A Sequence 4, A
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-733-320-4

US-08-733-326-15

US-08-733-326-2

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US-08-465-248-27

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Maximum Match 100%
Listing first 45 summaries
                                      protein search, using sw model
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1 NTTIGVFGLKQDWDGATIKD 20
                                                          March 14, 2002, 09:07:38
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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APPLICANT: Nyika, Aceme
APPLICANT: Rurangirwa, Fred R.
APPLICANT: Rurangirwa, Fred R.
APPLICANT: Rurangirwa, Fred R.
APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
TITLE OF INVENTION: Animals and Humans
FILE REFERENCE: UP-1670!
CURRENT APPLICATION NUMBER: US/08/953,326
BARLIER PELLING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/733,230
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Pred. No. 4.5e-07;
1; Mismatches 1; Indels
                                                                                        US-08-446-600A-4
US-09-413-231-6
US-09-413-231-7
US-08-586-165-3
US-08-586-165-5
US-08-694-2
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US-08-366-490-2
US-08-366-490-6
                        US-09-034-306-4
US-09-259-437-4
PCT-US93-09782-4
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US-08-953-326-18
Sequence 18, Application US/08953326
Patent No. 6221872
GENERAL INFORMATION:
APPLICANT: Barbet, Anthony F.
APPLICANT: Mandar, Roman R.
APPLICANT: McGuire, Travis C.
APPLICANT: Murridge, Michael J.
APPLICANT: Nuika, Aceme
APPLICANT: Rurangirwa, Fred R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17, Application US/08953326
Patent No. 6251872
GENERAL INPORMATION:
APPLICANT: Barbet, Anthony F.
APPLICANT: Ganta, Roman R.
APPLICANT: McGuire, Travis C.
APPLICANT: Burridge, Michael J.
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US-08-953-326-17
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  US-08-953-326-17
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SEQ ID NO 17
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APPLICANT: Mahan, Suman M.

TITLE OF INVENTION: NUCLEIC ACID Vaccines Against Rickettsial Diseases of TITLE OF INVENTION: NUCLEIC ACID Humans
FILE REPERENCE: UF-167C1
CURRENT APPLICATION NUMBER: US/08/953,326
EARLIER APPLICATION NUMBER: 08/953,326
EARLIER APPLICATION NUMBER: 08/953,326
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-17
NUMBER OF SEQ ID NOSE: 24
SEQ ID NOS: 24
ENGINE PLAND NOSE: 24
ENGINE PLAND NOSE: PARENTIN VET. 2.0
EARLIER FILING SECOND NOSE: 24
ENGINE PLAND NOSE: PARENTIN VET. 2.0
ENGINE PLAND NOSE: PARENTIN VET. 2.0
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sequence No. 6029338

septicant: Barbet, Anthony F. APPLICANT: Ganta, Roman Reddy APPLICANT: Ganta, Roman Reddy APPLICANT: Ganta, Aceme APPLICANT: Mixa, Aceme APPLICANT: Wilka, Aceme APPLICANT: Wahan, Suman M. TITLE OF INVENTION: Nucleic Acid Vaccines Against TITLE OF INVENTION: Use STORESS: ADDRESSEE: Saliwanchik & Saliwanch & S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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; ORGANISM: Ehrlichia chaffeensis
US-08-953-326-18
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SEQUENCE CHARACTERISTICS:
SEQUENCE: 280 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein.
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US-08-733-230-4
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       Length 280;
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Query Match 74.5%; Score 82; DB 3; Length 280
Best Local Similarity 70.0%; Pred. No. 8.9e-06;
Matches 14; Conservative 3; Mismatches 3; Indels
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; ORGANISM: Ehrlichia chaffeensis
US-08-953-326-4
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GENERAL INFORMATION:
APPLICANT: Barbet, Anthony F.
APPLICANT: Ganta, Roman R.
APPLICANT: Ganta, Roman R.
APPLICANT: Gure, Travis C.
APPLICANT: Burridge, Michael J.
APPLICANT: Burridge, Michael J.
APPLICANT: Nyika, Aceme
APPLICANT: Nyika, Aceme
APPLICANT: Nyika, Aceme
TITLE OF INVENTION: Wucleic Acid Vaccines Against Rickettsial Diseases of
TITLE OF INVENTION: Animals and Humans
TITLE OF INVENTION: Animals and Humans
TITLE OF INVENTION: MUMBER: US/08/953,326
CURRENT APPLICATION NUMBER: US/08/953,326
CURRENT FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/953,336
EARLIER PLING DATE: 1997-10-17
EARLIER PLING DATE: 1997-10-17
EARLIER PLING DATE: 1996-10-17
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FREATL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Barbet, Anthony F.
APPLICANT: Buriday. Michael J.
APPLICANT: Buriday. Michael J.
APPLICANT: Rurangirwa, Fred R.
APPLICANT: Nika, Aceme
APPLICANT: Alman M.
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
TITLE OF INVENTION: Animals and Humans
FILE REFERENCE: UF-167C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 59.5; DB 4; Length 287; Pred. No. 0.04;
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CURRENT FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/953,326
EARLIER FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/733,230
                         Sequence 2, Application US/08953326
Patent No. 6251872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Ehrlichia chaffeensis
US-08-953-326-16
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NUMBER OF SEO ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 278
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; ORGANISM: Cowdria ruminantium
US-08-953-326-2
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60.09
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 80.0
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
US-08-953-326-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 2
LENGIH: 287
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                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rurangirwa, Fred R.
APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Nucleic Acid Vaccines Against
TITLE OF INVENTION: Rickettsial Diseases and Methods of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 59.5; DB 3; Length 287;
Pred. No. 0.04;
1; Mismatches 1; Indels
                                                                                                                                                    Score 71; DB 4; Length 286;
Pred. No. 0.00055;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,230
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Saliwanchik & Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Barbet, Anthony F.
APPLICANT: Ganta, Roman Reddy
APPLICANT: McGuire, Travis C.
APPLICANT: Burridge, Michael J.
APPLICANT: Nyika, Aceme
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08733230 Patent No. 6025338
                                      TYPE: PRT; ORGANISM: Ehrlichia chaffeensis US-08-953-326-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 352-375-8100
                                                                                                                                                    64.5%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 2:
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80.0%;
                                                                                                                                                                                                                                          1 NTTTGVFGLKQDWDGATI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 287 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                    60 NTTVGVFGIEQDWDRCVI 77
                                                                                                                                                 Query Match
Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         352-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-733-230-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 NTTTGVFGLKQDWDG 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
SEQ ID NO 15
LENGTH: 286
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US-08-733-230-2
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1 NTTTGVFGLKQDWDG 15

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Sequence 2, Application US/08991942

Sequence 2, Application US/08991942

Patent No. 6015673

GENERAL INCEMATION

GENERAL INCORMATION

APPLICANT: FERNANDEZ-SALGUERO, PEGTO

TITLE OF INVENTION: CLONING AND EXPRESSION OF CDNA FOR HUMAN

TITLE OF INVENTION: CLONING AND EXPRESSION OF CONR FOR HUMAN

TITLE OF INVENTION: CLONING AND EXPRESSION OF CONR FOR HUMAN

TITLE OF INVENTION: DIPTORPREDIATE DEHYDROGENASE

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSE: Townsend and Townsend Khourie and Crew

STRRET: Steuart Street Tower, One Market Plaza

CITY: San Francisco

STREE: California

COUNTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: BLOPPY disk

COMPUTER: PALOS-NAS-DOS

SORFWARPE: POSS-NAS-DOS

SORFWARPE: POSS-NAS-DOS-NAS-DOS

SORFWARPE: POSS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NAS-DOS-NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.8%; Score 40.5; DB 2; Length 1025; 42.9%; Pred. No. 2.1e+02; tive 2; Mismatches 7; Indels 3.
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SOCTAMER: IBM PC COMPATIBLE
SOCTAMER: Patentin Release #1.0, Version #1.25
SOCTAMER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,942
FILING DATE: US/08/991,942
FILING APPLICATION NUMBER: US/08/304,309
FILING DATE: 09-SEP-1994
ATTORNEY/AGENT INFORMATION:
RAME: Smith, Timothy L.
REGISTRATION NUMBER: 15.280-210
FELEPHONE: (415) 543-960
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF $43-960
TELECOMMUNICATION OF $23-560
TELECOMUNICATION OF $23-560
TELECOMMUNICATION OF $23-560
TELECOMMUNICATI
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Pred. No. 2.1e+02;
2; Mismatches 7;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-560
TELEFAX: (415) 543-5603
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1025 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NTTTGVFGLKQD---WDGATI 18
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Best Local Similarity 42.9%;
Matches 9; Conservative
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Best Local Similarity 42.9
Matches 9; Conservative
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TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-991-942-2
                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-304-309-2
                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
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US-08-991-942-2
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GENERAL INFUGRATION
GENERAL INFUGRATION
APPLICANT: Barbet, Anthony F.
APPLICANT: Ganta, Roman R.
APPLICANT: McGuire, Travis C.
APPLICANT: WcGuire, Travis C.
APPLICANT: Wahan, Suman M.
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
CURRENT FILING DATE: 1997-10-17
SEALLER PILING DATE: 1997-10-17
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 20
SEQ ID NO 20
SEQ ID NO 20
LENGTH: 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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| Sequence 2, Application US/08304309
| Patent No. S856454
| GENERAL INFORMATION:
| APPLICANT: GONZALEZ, Frank J.
| TITLE OF INVENTION: DIHYDROPYRIMIDINE DEHYDROGENASE
| TITLE OF INVENTION: DIHYDROPYRIMIDINE DEHYDROGENASE
| ADDRESSEE: Townsend and Townsend khourie and Crew
| STREET: Steuart Street Tower, One Market Plaza
| CITY: San Francisco |
| COUNTRY: US
| COUNTRY: US
| CONFUTER READABLE FORM: |
| MEDIUM TYPE: Floppy disk |
| COMPUTER: IBM PC compatible |
| CONFUTER: IBM PC compatible |
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44.5%; Score 49; DB 4; Length 133;
Best Local Similarity 56.2%; Pred. No. 0.82;
Matches 9; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                   RESULT 9
US-08-953-326-20
Sequence 20, Application US/08953326
Patent No. 6251872
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Ehrlichia canis
US-08-953-326-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 TTGVFGLKQDWDGATI 18
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            60 NPTVALYGLKODWEG 74
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Gaps

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us-09-765-739a-2.rai

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NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                                                           1 NTTTGVFGLKQD---WDGATI 18
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Best Local Similarity 41.2%;
Matches 7; Conservative
LENGTH: 1025 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 TGVFGLKQDWDGATIKD 20
                                                                                                                                                                        Best Local Similarity 42.9
Matches 9; Conservative
                             ; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-04567-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                         amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 2
LENGTH: 523
                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
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                                                                         Sequence 2, Application US/09138103A

Patent No. 6232448

GENERAL INFORMATION:
APPLICANT: Yoshikubo, Takashi
APPLICANT: Hasegawa, Masami
TITLE OF INVENTION: Inmunological Materials and Methods for Detecting
TITLE OF INVENTION: Inmunological Materials and Methods for Detecting
TITLE OF INVENTION: Dihydropyrimidine Dehydrogenase
FILE REFERENCE: 09/138,103 Yoshikubo, et al.
CURRENT FILING DATE: 1998-08-138,103A

CURRENT FILING DATE: 1998-08-22

BARLIER TILING DATE: 1997-08-22

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application PC/TUS9504567
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE
TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE
NUMBER OF SEQUENCES: 28
CORRESPONDENCES: 28
CORRESPONDENCES: Annold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.8%; Score 40.5; DB 4; 142.9%; Pred: No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version SOFTWARE: #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMER: PCT/US95/04567
FILING DATE: CONCURRENTLY HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Vers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UOAB025P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,357
FILING DATE: 13-APR-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: WILSON, MARK B.
REGISTRATION NUMBER: 37,259
REFRENCE/DOCKET NUMBER: UOAB
TELECOMMUNICATION INFORMATION:
TELEPAN: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 736 NTVSGLMGLKSDGTPWPAVGI 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NTTTGVFGLKQD---WDGATI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 42.57
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens US-09-138-103-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: CC
                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 2
LENGTH: 1025
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                                                      US-09-138-103-2
                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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; ORGANISM: Brevibacterium lactofermentum (Corneybacterium glutamicum)
US-09-550-338-2
                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: KAMASARI, Hisashi
APPLICANT: USUDA, YOShihiro
APPLICANT: MIHARA, YOShihiro
APPLICANT: KURAHASHI, Osamu
TITLE OF INVENTION: GMP Synthetase and Gene Coding for the Same
FILE REFERENCE: 0010-1101-0
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  Length 1025;
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                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 4; Le
Pred. No. 1.1e+02;
4; Mismatches 6;
36.8%; Score 40.5; DB 5; 42.9%; Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STAFF: New York
COMTRY: United States of America
ZIP: 11530
                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/550,338
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: JP 11-114787
PRIOR FILING DATE: 1999-04-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08828741B Patent No. 6043069 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriale M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
                                                                                                                                                                                                                                      US-09-550-338-2; Sequence 2, Application US/09550338; Patent No. 6210951
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Search completed: March 14, 2002, 09:07:39 Job time: 840 sec

us-09-765-739a-2.rag

Page 1

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E. canis P30 prote
E. chafeensis OMP-
Ehrlichia chaffeen
Variable surface a
E. chafeensis p28
Ehrlichia chaffeen
Ehrlichia chaffeen
Fariable surface a
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13.281 Million cell updates/sec
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                                                                                                                March 14, 2002, 09:09:36; Search time 111.55 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1984.DAT:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                  522463 seqs, 74073290 residues
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Maximum Match 100%
Listing first 45 summaries
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AAB36188
AAU04198
AAY06942
AAW51095
AAW04199
AAW51089
AAW51089
                                                                           OM protein - protein search, using sw model
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1 NTTTGVFGLKQDWDGATIKD 20
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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В
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ALIGNMENTS

Major antigenic pr E. chafeensis OMP- E. canis P30-2 pro Ehrlichia canis im E. canis P30-4 pro E. chafeensis CAMP- E. chafeensis CAMP-	En Chartenists Officer Ehrlichia chaffeen Variable surface a Ehrlichia canis im E. canis P30-1 pro Cowdria ruminantiu Major antigenic pr Ehrlichia chaffeen	E. chafeensis OMP- Ehrlichia chaffeen Variable surface a E. chafeensis OMP- Variable surface a Ehrlichia canis ya Ehrlichia canis im Ehrlichia canis im	Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Sensocence-associa
AAU04193 AAY06943 AAY06962 AAY1479 AAX06964 AAX06964	AAB3618 AAB3618 AAY7147 AAY70696 AAW5108 AAB3618 AAW5109		
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82 77 77 76	71 71 70 70 59.5 59.5 59.5	. W W W W 4 4 4 4 4	\$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$
112 114 115 116	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	3 3 3 3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30; ¥. AAY06959 standard; Protein; 288 (first entry) E. canis P30 protein. Ehrlichia canis. detection; dog WO9913720-A1. 05-JUL-1999 25-MAR-1999 AAY06959; AAY06959 RESULT

97US-0059353. (OHIS.)-UNIV-OHIO-STATE Ohashi N, Rikihisa Y; WPI; 1999-254290/217 N-PSDB; AAX34759. 19-SEP-1997;

98WO-US19600.

18-SEP-1998;

Novel outer membrane proteins from Ehrlichia chaffeensis and Ehrlichia canis

Disclosure; Fig 19B; 55pp; English

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Composition containing nucleic acid encoding fickettsial antigen - useful for, e.g. stimulating protective immune response in humans or animals
                                                                                                                                                            MAP1 homologue; variable surface antigen; VSA4; rickettsia;
                                                                                                                             Ehrlichia chaffeensis VSA4 protein.
                                AAW51094 standard; Protein; 280 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Fig 2B; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barbet AF, Burridge MJ,
Nyika A, Rurangirwa FR;
                                                                                                                                                                                                          Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                            (UYFL ) UNIV FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-251232/22.
N-PSDB; AAV07179.
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                                                                                                                                                                                                                                                                                                                                                                17-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                               17-OCT-1996;
                                                                                              14-SEP-1998
                                                                                                                                                                               DNA vaccine.
                                                                                                                                                                                                                                                                                                                                   23-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barbet AF,
                                                               AAW51094;
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Peptide
 RESULT
AAW51094
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The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafebensis and E. canis. The E. chafebensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to 2) shown in AAY06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAY06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention provides isolated outer membrane proteins (OMP) from Entlinia chafeensis and E. canis. The E. chafeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in AAY06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAY06959-970. The proteins and genes are used to detect E. chafeensis in patients and E. canis in dogs.
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30;
                                                                                                                                                                                          ö
                                                                                                                                                         Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel outer membrane proteins from Ehrlichia chaffeensis and Ehrlichia canis
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                                                                                                                                                                                          Indels
                                                                                                                                                       Ouery Match 100.0%; Score 110; DB 20; Best Local Similarity 100.0%; Pred. No. 9.9e-10; Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                               AAY06948 standard; Protein; 280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 16; Fig 8B; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            E. chafeensis OMP-1F protein.
                                                                                                                                                                                                                       1 NTTTGVFGLKQDWDGATIKD 20
                                                                                                                                                                                                                                         87.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-US19600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97us-0059353.
                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 87.33
Best Local Similarity 94.43
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (OHIS ) UNIV OHIO STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohashi N, Rikihisa Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ehrlichia chafeensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-254290/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAX34748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09913720-A1.
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                                                                                                                                                                                                                                                                                                                                                              AAY06948;
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                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                  RESULT
AAY06948
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Ganta RR, Mahan SM, McGuire TC;

1..25 /note= "putative signal peptide"

97WO-US19044.

96US-0733230.

Location/Qualifiers

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This is the full-length variable surface antigen VSA4 protein of Bhrilchia draffeensis. Its amino acid sequence was deduced from a partial open reading frame (ORF4) of a genomic locus (see AAV07179) of E. chaffeensis that was obtained on the basis of homology to the major antigence protein MAP1 (see AAW51088) of Cowdria ruminantium. This genomic locus included 5 ORFs encoding similar, but non-identical proteins (see AAW51091-95). A claimed composition comprises a nucleic acid (see AAW071076-82) encoding a polypeptide (see AAW51088-99) that elicits a protective immune response against rickettsial pathogen. The nucleic acid is used, in human or veterinary medicine, in vaccines to protect against Rickettsia. Britichia, Anaplasma and Cowdria species. The Birlichia antigenic associated with Ehrlichia Infection (claimed).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 90; DB 19; Length 28
Pred. No. 1.5e-06;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81.8%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NTTTGVFGLKQDWDGATI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 nttigvfglkqdwdgsti 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                          280 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB36188
ID AAB3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db
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Gaps

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1 NTTTGVFGLKODWDGATI 18

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Nyika A;

McGuire TC, Burridge MJ, SM, Bowie MV, Alleman AR;

97US-0953326.

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Ehrlichia chaffeensis.
                                                                                                                                                  Barbet AF, Ganta RR,
Rurangirwa FR, Mahan
                                                                                                                             (UYFL ) UNIV FLORIDA.
                                  US6251872-B1.
                                                                               17-0CT-1997;
                                                                                                      17-0CT-1996;
                                                         26-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY06942
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                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence shows a high degree of similarity to the major antigenic protein 1 (MAP1) of Ehrlichia sp. The MAP1 gene may be used in a vaccines to protect animals or humans against rickettsial diseases caused by a organisms of Rickettsia sp., Ehrlichia sp., Anaplasma sp. or Cowdria sp. The vaccine elicits an immune response protective against the rickettsial pathogen. The nucleic acid vaccines can be driven by the human cytomegalovirus (HCMV) enhancer-promoter. Cowdria rumhnatium genes designated map 2, Ihworf3, 4hworf1, 18hworf1 and 3doorf3 may be used in therapeutic and disgnostic applications. The polypeptides are useful for detecting antibodies associated with infection by a rickettsial pathogen whilst the polynucleotides may be used to detect the presence of rickettsial nucleic acids.
                                                                                                                                                                                                                                                                                                                                   New polynucleotides useful as DNA vaccines for conferring immunity to rickettsial infection e.g. heartwater caused by Cowdria ruminantium, comprises major antigenic protein 1 or 2 gene of rickettsial pathogens
                                                                                                                                                                                                                                                                   McGuire TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                        Mahan SM, Mcca.
- wW, Alleman AR;
                                                                Ehrlichia chaffeensis; VSA4; variable surface antigen 4; MAP1; major antigenic protein 1; antirickettsial; vaccine; gene therapy; Rickettsia; Cowdria; Anaplasma; map2; lhworf3; 4hworf1; 18hworf1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Major antigenic protein; MAP; vaccine; immunogenic; rickettsia; infection; heartwater; diagnostic; variable surface antigen; VSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Variable surface antigen 4 (VSA4) from Ehrlichia chaffeensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 90; DB 21; Length 280;
Pred. No. 1.5e-06;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                 Ganta RR, Burridge MJ, Mahan
nd AL, Simbi BH, Whitmire WW,
                                            Ehrlichia chaffeensis partial VSA4.
                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 45-46; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU04198 standard; Protein; 280 AA.
                                                                                                                                                                                                                                                                  Barbet AF, Bowie MV, Ganta
Rurangirwa FR, Moreland AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.8%;
88.9%;
                                                                                                                                                                                             21-APR-2000; 2000WO-US10886
                                                                                                                                                                                                                      99US-0130725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NTTTGVFGLKQDWDGATI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16; Conservative
                                                                                                                          Ehrlichia chaffeensis.
                                                                                                                                                                                                                                           (UYFL ) UNIV FLORIDA
                                                                                                                                                                                                                                                                                                 WPI; 2000-679675/66.
N-PSDB; AAC68705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 AA;
                                                                                                                                                 WO200065063-A2
                                                                                                                                                                                                                      22-APR-1999;
                    02-MAR-2001
                                                                                                                                                                        02-NOV-2000
                                                                                                                                                                                                                                                                Barbet AF,
AAB36188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU04198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU04198
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                                                                                                                                                                                                                                                                                                     antigen 4 (YSA4) isolated from Ehrlichia chaffeensis, which has similarity to major antigen protein (MAP). The MAP polynuclectides and polypeptides are useful as vaccines for conferring immunity to rickettsia infection, including Cowdria ruminantium causing heartwater. The MAP polynuclectides may be used as molecular markers in nucleic acid analysis procedures, and to produce the MAP polypeptides, which may be used to raise antibodies that are reactive with the polypeptides. The nucleic acids may further be used as probes to identify complementary sequences within other nucleic acid molecules or genomes, where such probes can be applied to identify or distinguish infectious strains of organisms in diagnostic procedures or in rickettsial research where identification of particular organisms or strains is
                                                                                                                               heartwater, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                  The sequence represents the amino acid sequence of variable surface
                                                                                         New MAP2 genes and polypeptides useful as vaccines for conferring immunity to human and animal rickettsial diseases, e.g. heartwater as molecular markers in nucleic acid analysis procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 90; DB 22; Le
Pred. No. 1.5e-06;
1; Mismatches 1;
                                                                                                                                                                                                                     Example 3; Fig 2A-2B; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY06942 standard; Protein; 256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.8%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US19600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NTTTGVFGLKQDWDGATI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E. chafeensis p28 protein.
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WPI; 2001-424487/45.
N-PSDB; AAS07578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detection; dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09913720-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY06942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
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22-APR-1999;
                                                                                                                                                                                                                                                                                           02-MAR-2001
                                                                                                                                            Sednence
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                                                                                                                                                                                                                                                   AAB36189
                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                            Db
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                                                                                                                The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafebensis and E. canis. The E. Chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to 2) shown in AAYO6943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAYO6959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Composition containing nucleic acid encoding rickettsial antigen - useful for, e.g. stimulating protective immune response in humans or animals
                                                                                                                                                                                                                   ;
0
                                                                       Novel outer membrane proteins from Ehrlichia chaffeensis and Ehrlichia canis
                                                                                                                                                                                                 Length 256;
                                                                                                                                                                                                                                                                                                                                                          MAP1 homologue; variable surface antigen; VSA5; rickettsia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McGuire TC;
                                                                                                                                                                                                 74.5%; Score 82; DB 20; Length 25. 70.0%; Pred. No. 2.6e-05; 1ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                           Ehrlichia chaffeensis VSA5 protein (partial sequence).
                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers .
1..25
/note= "putative signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mahan SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ganta RR,
                                                                                                                                                                                                                                                                                          AAW51095 standard; Protein; 276 AA.
                                                                                                  Claim 18; Fig 1; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Fig 2B; 39pp; English
                                                                                                                                                                                                                                  1 NTTTGVFGLKQDWDGATIKD 20
                                                                                                                                                                                                                                           97us-0059353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-US19044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0733230
                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                Query Match
Best Local Similarity 70.0°
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Burridge MJ,
                (OHIS ) UNIV OHIO STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barbet AF, Burridge MJ
Nyika A, Rurangirwa FR;
                                Ohashi N, Rikihisa Y;
                                                                                                                                                                                                                                                                                                                                                                                   Ehrlichia chaffeensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYFL ) UNIV FLORIDA.
                                                WPI; 1999-254290/21.
N-PSDB; AAX34742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-251232/22.
N-PSDB; AAV07179.
                                                                                                                                                                          256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9816554-A1
19-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-OCT-1996;
                                                                                                                                                                                                                                                                                                                          14-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-APR-1998
                                                                                                                                                                                                                                                                                                                                                                     DNA vaccine
                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                           AAW51095;
                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
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                                                                                                                                                                                                                                                                                  AAW51095
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This is the near full-length variable surface antigen VSA5 protein of Ehrlichia chaffeensis; it lacks about 5-7 C-terminal amino acid sequence was deduced from a partial cresidues. The VSA5 antion acid sequence was deduced from a partial open reading frame (ORF5) of a genomic locus (see AAV07179) of E. chaffeensis that was obtained on the basis of homology to the major antigenic protein MAP1 (see AAM51088) of Cowdria ruminantium. This genomic locus included 5 ORFs encoding similar but non-identical proteins (see AAM07176-82) encoding a polypeptide (see AAM51088-99) that elicits a protective immune response against a rickettsial medicine, in vaccines to protect against Rickettsia Enrichia, medicine, in vaccines to protect against Rickettsia. Ehrlichia, analysma and Cowdria species. The Ehrlichia antigenic polypeptides can be used diagnostically to detect antibodies associated with Ehrlichia infection (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotides useful as DNA vaccines for conferring immunity to rickettsial infection e.g. heartwater caused by Cowdria ruminantium, comprises major antigenic protein 1 or 2 gene of rickettsial pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barbet AF, Bowie MV, Ganta RR, Burridge MJ, Mahan SM, McGuire TC;
Rurangirwa FR, Moreland AL, Simbi BH, Whitmire WW, Alleman AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence shows a high degree of similarity to the major antigency protein 1 (MAPI) of Ehrlichia sp. The MAPI gene may be used in a vaccines to protect animals or humans against rickettsial diseases caused by a organisms of Rickettsia sp., Ehrlichia sp.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ehrlichia chaffeensis; VSA5; variable surface antigen 5; MAP1; major antigenic protein 1; antirickettsia1; vaccine; gene therapy; Rickettsia; Cowdria; Anaplasma; map2; 1hworf3; 4hworf1; 18hworf1; 3gdorf3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.5%; Score 82; DB 19; Length 276; 70.0%; Pred. No. 2.9e-05; ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB36189 standard; Protein; 276 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 70.0
Matches 14; Conservative
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N-PSDB; AAC68706.
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276 AA;

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Sequence
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                                                                                                                                                                        AAW51089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence represents the amino acid sequence of variable surface antigen 5 (VSA5) isolated from Ehrlichia chaffeensis, which has similarity to major antigen protein (MAP). The MAP polynucleotides and polypeptides are useful as vaccines for conferring immunity to rickettsia infection, including Cowdria ruminantium causing heartwater. The MAP polynucleotides may be used as molecular markers in nucleic acid analysis procedures, and to produce the MAP polypeptides, which may be used to raise antibodies that are reactive with the polypeptides. The nucleic acids may further be used as probes to identify complementary sequences within other nucleic acid molecules or genomes, where such probes can be applied to identify or distinguish infectious strains of organisms in diagnostic procedures or in rickettsial
Anaplasma sp. or Cowdria sp. The vaccine elicits an immune response protective against the rickettsial pathogen. The nucleic acid vaccines can be driven by the human cytomegalovirus (HCMV) enhancer-promoter. Cowdria ruminatium genes designated map 2, hhworf1, 18hworf1 and 3fdorf3 may be used in therapeutic and diagnostic applications. The polypeptides are useful for detecting antibodies associated with infection by a rickettsial pathogen whilst the polynucleotides may be used to detect the presence of rickettsial nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New MAP2 genes and polypeptides useful as vaccines for conferring immunity to human and animal rickettsial diseases, e.g. heartwater, or as molecular markers in nucleic acid analysis procedures
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           Major antigenic protein; MAP; vaccine; immunogenic; rickettsia; infection; heartwater; diagnostic; variable surface antigen; VSA.
                                                                                                                                                                                    .
,
                                                                                                                                                                                                                                                                                                                                                                                  Variable surface antigen 5 (VSA5) from Ehrlichia chaffeensis.
                                                                                                                                                         DB 21; Length 276; 2.9e-05; ches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nyika A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McGuire TC, Burridge MJ,
SM, Bowie MV, Alleman AR;
                                                                                                                                                                                    Mismatches
                                                                                                                                                          Score 82;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Fig 2A-2B; 30pp; English.
                                                                                                                                                                                                                                                                                                      AAU04199 standard; Protein; 276 AA.
                                                                                                                                                          74.5%;
70.0%;
                                                                                                                                                                                                            1 NTTTGVFGLKQDWDGATIKD 20
                                                                                                                                                                                                                             97US-0953326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96US-0733230
                                                                                                                                                                                                                                                                                                                                                       23-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barbet AF, Ganta RR, McG
Ruranqirwa FR, Mahan SM,
                                                                                                                                                                                   14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                Ehrlichia chaffeensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYFL ) UNIV FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-424487/45.
                                                                                                                                                         Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                     276 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAS07578
                                                                                                                                                                                                                                                                                                                                                                                                           Major antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-0CT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6251872-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUN-2001.
                                                                                                                                                                                                                                                                                                                                AAU04199;
                                                                                                                     Sequence
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                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This polypeptide comprises the major antigen protein I gene (MAPI) of Ehrlichia chaffeensis. It is encoded by the MAPI gene (see AAV01777). A claimed composition comprises a nucleic acid (see ARV07176-82) encoding a polypeptide (see AAW51088-99) that elicits a protective immune response against a rickettsial pathogen. The nucleic acid is used, in human or veterinary medicine, in vaccines to protect against Ricketsia. Brilichia, Anaplasma and Cowdria species. The nucleic acid does not replicate in the host but remains episomal and capable of expressing polypeptide for at least 19 mth. The Ehrlichia antigenic polypeptides can be used diagnostically to detect antibodies associated with Ehrlichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition containing nucleic acid encoding rickettsial antigen - useful for, e.g. stimulating protective immune response in humans or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAP1 gene; major antigenic protein 1; rickettsia; DNA vaccine
                     Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McGuire TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 280;
Score 82; DB 22; Lengtn 2/v
Pred. No. 2 9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Ehrlichia chaffeensis major antigenic protein 1 (MAP1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74.5%; Score 82; DB 19; L. 70.0%; Pred. No. 2.9e-05; iive 3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mahan SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ganta RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 18-19; 39pp; English.
                                                                                                                                                                                                                                                                     AAW51089 standard; Protein; 280 AA.
                                                             3;
                     74.5%;
70.0%;
                                                                                                            20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97WO-US19044.
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                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                            1 NTTTGVFGLKQDWDGATIKD
                                                                                                                                   Conservative
                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nyika A, Rurangirwa FR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ehrlichia chaffeensis.
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                     Query Match
Best Local Similarity
Matches 14; Conserv
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Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-0CT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barbet AF,
                                                                                                                                                                                                                                                                                                                 AAW51089;
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Nyika A;

97US-0953326: 96US-0733230.

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New MAP2 genes and polypeptides useful as vaccines for conferring immunity to human and animal rickettaial diseases, e.g. heartwater, or as molecular markers in nucleic acid analysis procedures
                                               Major antigenic protein 1; MAP1; vaccine; immunogenic; rickettsia;
infection; heartwater; diagnostic.
                        Major antigenic protein 1 (MAP1) from Ehrlichia chaffeensis.
                                                                                                                                                                                                                                  Barbet AF, Ganta RR, McGuire TC, Burridge MJ,
Rurangirwa FR, Mahan SM, Bowie MV, Alleman AR;
                                                                                                                                                                                                                                                                                                                                                          Disclosure; Column 15-17; 30pp; English.
                                                                                   Ehrlichia chaffeensis.
                                                                                                                                                                                                           (UYFL ) UNIV FLORIDA.
                                                                                                                                                                                                                                                                     WPI; 2001-424487/45.
N-PSDB; AAS07576.
                                                                                                           US6251872-B1.
                                                                                                                                                            17-OCT-1997;
                                                                                                                                                                                   17-OCT-1996;
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                                                                                                                        Ehrlichia chaffeensis; MAPI; major antigenic protein 1; antirickettsial;
Vaccine; gene therapy; Rickettsia; Cowdria; Anaplasma; map2; 1hworf3;
4hworf1; 18hworf1; 3gdorf3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is given in a specification relating to nucleic acid vaccines containing genes to protect animals or humans against rickettsial diseases caused by a organisms of Rickettsial as pp., Ehrlichia protective against the rickettsial pathogen. The vaccine comprises the protective against the rickettsial pathogen. The vaccine comprises the major antigenic protein 1 (MAP2) gene or the major antigenic protein 2 for the major antigenic protein and against the major and polypeptides are used in therapeutic and diagnostic applications. The infection by a rickettsial pathogen whilst the polypuclectides may be used to detecting antibodies associated with used to detect the presence of rickettsial nucleic acids.
                                                                                                                                                                                                                                                                                                                               Ganta RR, Burridge MJ, Mahan SM, McGuire TC;
nd AL, Simbi BH, Whitmire WW, Alleman AR;
                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides useful as DNA vaccines for conferring immunity to rickettsial infection e.g. heartwater caused by Cowdria ruminantium, comprises major antigenic protein 1 or 2 gene of rickettsial pathogens
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No. 2.9e-05;

Matches 14; Conservative 3; Mismatches 3; Indels
                         AAB36183 standard; Protein; 280 AA.
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AAU04193
XX AAU04193 standard; Protein; 280 AA.
AC AAU04193;
XX XX
XX XX
XX XX
AC AAU04193;
                                                                                                                                                                                                                                                                                                                            Bowie MV, Ganta
FR, Moreland AL,
                                                                                                                                                                                                                                                   21-APR-2000; 2000WO-US10886.
                                                                                                  Ehrlichia chaffeensis MAP1.
                                                                                                                                                                                                                                                                            99US-0130725
                                                                          02-MAR-2001 (first entry)
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                                                                                                                                                                                                                                                                                                  (UYFL ) UNIV FLORIDA.
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N-PSDB; AAC68700.
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                                                                                                                                                                                                  WO200065063-A2.
                                                                                                                                                                                                                                                                                                                        Barbet AF, Bow
Rurangirwa FR,
                                                                                                                                                                                                                                                                           22-APR-1999;
                                                                                                                                                                                                                            02-NOV-2000
                                                   AAB36183;
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The sequence represents the amino acid sequence of major antigenic polypeptides are useful as vaccines for conferring immunity to rickettsia polypeptides are useful as vaccines for conferring immunity to rickettsia infection, including Cowdria ruminantium causing heartwater. The MAP polynuclectides may be used as molecular markers in nucleic acid pelanguis procedures, and to produce the MAP polypeptides, which may run and to produce the MAP polypeptides, which may rooplementary sequences within other nucleic acid molecules or dentify where such probes can be applied to identify or distinguish infectious research where identification of particular organisms or strains is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NTTTGVFGLKQDWDGATIKD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E. chafeensis OMP-1 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                      280 AA;
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Gaps

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The patent relates to homologous 28-kiloDalton (kDa) protein genes of Ehrlichia canis, designated ECa28SA1, ECa28SA3, ECa28SA3, ECa28SA3, ECa28SA3, ECa28SA3, ECa28SA2, ECA28SA3, ECA28SA2, ECA28SA3, ECA28SA3, ECA28SA2, ECA28SA3, ECA38SA3, ECA38SA3
of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in AAY06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAV06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homologous 28-kDa protein gene; ECa28SA3; immunoreactive; vaccine; p28 gene; polymorphic multiple gene family; immunoprotective antigen; antibacterial; canine ehrlichiosis; canine tropical pancytopaenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ehrlichia canis antigens useful for vaccinating against canine ehrlichiosis in dogs -
                                                                                                                                                                                                            Length 280;
                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24..280
/label= Mature_ECa28SA3_28-kDa_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ehrlichia canis immunoreactive protein ECa28SA3.
                                                                                                                                                                                                          70.0%; Score 77; DB 20;
65.0%; Pred. No. 0.00018;
ive 3; Mismatches 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tick-borne rickettsial disease; serodiagnosis.
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/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY71479 standard; Protein; 280 AA.
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59 nstvgvfglkhdwnggtisn 78
                                                                                                                                                                                                                                                                                                                1 NTTTGVFGLKQDWDGATIKD 20
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99US-0261358.
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                                                                                                                                                                                                                                    Best_Local Similarity 65.0
Matches 13; Conservative
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                                                                                                                              280 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ehrlichia
                                                                                                                                   Sequence
                                                                                                                                                                                                            Query Match
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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ehrlichia chafeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to 2) shown in AAY06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAY06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins (OMP) from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                outer membrane proteins from Ehrlichia chaffeensis and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 82; DB 20; Length 281;
Pred. No. 2.9e-05;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention provides isolated outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY06962 standard; Protein; 280 AA.
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70.0%;
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                                                                           97US-0059353.
                          98WO-US19600
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Best Local Similarity 70...
Local 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (OHIS ) UNIV OHIO STATE.
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                                                                                                                                                                               Ohashi N, Rikihisa Y;
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AAY06962;

AAY06962

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Sequence

Novel

mature 28-kDa protein by cleavage of N-terminal signal sequence.

Sequence 280 AA;

Query Match
Best Local Similarity 65.0%; Score 77; DB 21; Length 280;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps
Qy 1 NTTGVFGLKQDWDGATIKD 20
Db 59 nstrgvfglkhdwnggtisn 78

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Search completed: March 14, 2002, 09:09:37 Job time: 428 sec

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"Molecular cloning of the gene for a conserved major immunoreactive
28 kilodalton protein of Ehrlichia canis: a potential serodiagnostic
                                                                                    cowdria
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MEDLINE-98371112; PubMed-9705412;

Ohashi-N., Unver A., Zhi N., Rikihisa Y.;

Cloning and Characterization-of-multigenes encoding the immunodominant 30 kilodalton major outer membrane proteins of Ehrlichia canis and application of the recombinant protein for serodiagnosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MCBLINE 2043.107; PubMed=10974556;
MCBride J.W., Yu X.J., Walker D.H.;
"A conserved, transcriptionally active p28 multigene locus of Ehrlichia canis.";
Ehrlichia canis.";
EMBL; AF078553; AAC68667:1; -.
EMBL; AF082744; AAG14362.1; -.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLRel. 17, Last annotation update)
01-JUN-2001 (TrEMBLRel. 17, Last annotation update)
P30 OR P28-8
Ehrlichta canis.
Bacteria: Proteobacteria; alpha subdivision; Rickettsiaceae, Ehrlichieae; Ehrlichieae; Ehrlichieae; Ehrlichieae
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MEDLINE=99242757; Pubmed=10225842;
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Q9zgj2 ehrlichia c
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Q8537 ehrlichia c
Q85817 ehrlichia c
O85817 ehrlichia c
Q9aci9 ehrlichia c
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pfam; PF01617; Surface_Ag_2; 1.
SEQUENCE 280 AA; 30743 MW; FBB841DAF08EE4DC CRC64;
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MEDLINE-98084465; PubMed-9423849;
Ohashi N., Zhing Y., Rikihisa Y.;
Immunodominant major outer membrane proteins of Ehrlichia chaffeensis are encoded by a pokymorphic multigene family.";
Infect. Immun. 66:132-139 1998).
EMBL: U72291; AAC02940-1:
InterPror: IPRO02566; Surface-A9_msp4.
Pfam: PF01617; Surface-A9_msp2.
Pfam: PF01617; Surface-A9_msp CRO64;
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Biochem. Biophys. Res. Commun. 247:636-643(1998).
EMBL. ARC62761; AAC26720.1; -.
InterPro; IPR002566; Surface_Ag_msp4.
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MEDLINE-98321180; PubMed-9647746;
Reddy G.R., Sulsona C.R., Barbet A.F., Mahan S.M., Burridge M.J.,
Alleman A.R.;
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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
NCBL_TasiD=945;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
28 KDA MAJOR SURRACE ANTIGEN-4.
Ehrlichia chaffeensis.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichiaee; Ehrlichia.
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Pred. No. 3e-07;
1; Mismatches 0; Indels
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InterPro; IPR002566; Surface_Ag_msp4.
Pfam; PF01617; Surface_Ag_2; Surfa
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STRAIN-ST.VICENT,
MEDINDE-99175287; Pubmed-10074538;
MEDINDE-99175287; Pubmed-10074538;
Yu X.J., MCBride J.W., Walker D.H.;
"Genetic diversity of the 28-kilodalton outer membrane protein gene in human isolates of Entlichta chaffeensis.";
J. Clin. Microbiol. 37:1137-1143(1999).
EMBL, AF07735, AAC31548.11
InterPro: IPR001702; Gram_neg_porin.
InterPro: IPR002566; Surface_Ag_msp4.
Pfam; PF01617; Surface_Ag_2: 1.
PRINTS, PR00182; ECONEIPORIN.
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I SEQUENCE 246 AA; 26884 MW; C9776392C5129A2F CRC64;
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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
NCBL_TaxID=945;
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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
NCBI_TaxID=945;
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STRAINE-SAPULBA;
Yu X.-J., Walker D.H.;
"Ehrlichia chaffeensis 28 kDa outer membrane protein.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL: AF077734; AAC3147-1; -
InterPro; IPR007566; Surface_Ag_msp4.
Pfam; PF0101; Surface_Ag_ST, 2PD36998FCFIF60BE CRC64;
SEQUENCE 276 AA: 30027 WW; 2PD3698FCFIF60BE CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
01-UNN-2001 (TREMBLRel. 17, Last annotation update)
01-UNN-2001 (TREMBRANE PROTEIN P28 PRECURSOR (FRAGMENT).
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1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                         "Molecular characterization of a 28 kDa surface antigen gene family of
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                               STRAIN=ARKANSAS;
BRDLINE-B8321180; PubMed=9647746;
Reddy G.R., Sulsona C.R., Barbet A.F., Mahan S.M., Burridge M.J.,
Alleman A.R.;
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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettslaceae; Ehrlichieae; Ehrlichia.
                                                                                                                                                                                               Ehrlichia chaffeensis.
Bacteria, Proteobacteria; alpha subdivision, Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
NCBI_TaxID-945;
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                  Length 276;
       Score 86; DB 2; Length 2/o
Pred. No. 1.1e-05;
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                                                                                                                                                               Last sequence update)
Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MAJOR OUTER MEMBRANE PROPEIN P28.
                                                                                                                                                                                                                                                                                                              the tribe Ehrlichiae.";
Biocham. Biophys. Res. Commun. 247:636-643(1998).
EMBL; AF062761; AAC26716.1;
ThiterPro: IPR002566; Surface_Ag_msp4.
Pfam; PF01677; Surface_Ag_2; 1.
NON_TER 276 276
                                                                                                                                   276 AA
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01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence to 01-JUN-2001 (TrEMBLrel. 17, Last annotation 28 KDA MAJOR SURFACE ANTIGEN-5 (FRAGMENT).
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MEDLINE=21153566; PubMed=11254561;
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MEDLINE=98084465; PubMed=9423849;
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                78.2%;
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                                                                      1 NTTTGVFGLKQDWDGATI 18
                                     Conservative
                                                                                                                                   PRELIMINARY;
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                Query Match
Best Local Similarity
Matches 15; Conserv
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Ohashi N., Rikihisa Y., Unver A.; "Analysis of Transcriptionally Active Gene Clusters of Major Outer Membrane Protein Multigene Family in Ehrlichia canis and E.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLR) PROTEIN P.28 PRECURSOR.
Ehrlichia chaffeensis.
Bacteria; Proteobacteria; alpha subdivision; Rickettsialess; Rickettsiaceae; Ehrlichiaee; Ehrlichia.
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Bacteria: Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
NCBI_TaxID=945;
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STRAIN=91HE17;

U. X.-J., Walker.

Functionia chaffeensis 28 kDa outer membrane protein.";

Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.

EMBL, AF077732; AAC31645.1;

Interpro; IPR002566; Surface_Ag_msp4.

Fram; PF01617; Surface_Ag_2; 1.

SEQUENCE 280 AA; 30277 MW; 91C54AC78507A63F CRC64;
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"Ehrlichia chaffeensis 28 kDa outer membrane protein.";
Submitted (Jul-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF077733; AAC31546.1;
InterPro: IPR002566; Surface_Ag_msp4.
Pfam; PF01617; Surface_Ag_2; J. Surface_Ag_Start 280 As; 30304 MW; 91C54AC7851B77F2 CRC64;
                                                                                                                 Infect. Immun, 69:2083-2091(2001).
EMBL; U72291; AAK28673.1; -.
SEQUENCE 281 AA; 30343 MW; A99E5F7C4459AA9A CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
00TER MEMBRANE PROTEIN P28 PRECURSOR.
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Length 280;

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MEDLINE-99242757; PubMed-10225842;
MCBAIde J.W. Yu, Xi, Walker D.H.;
"Molecular cloning of the gene for a conserved major immunoreactive
28-kilodalton protein of Ehrlichia canis: a potential serodiagnostic
                                                                                                                                                                        Obashi N., Rikihisa Y., Unver A.;
Analysis of Transcriptionally Active Gene Clusters of Major Outer
Membrane Protein Multigene Family in Ehrlichia canis and E.
Chaffeensis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE-20432107; PubMed-10974556;
MCBride J.W., Yu X.J., Walker D.H.;
"A conserved, transcriptionally active p28 multigene locus of
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Bacteria: Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
NCBL_TaxID=944;
Ohashi N., Unver A., Zhi N., Rikihisa Y.; Cloning and characterization of multigenes encoding the immunodominant 30-kilodalton major outer membrane proteins Ebrlichia canis and application of the recombinant protein serodiagnosis."; 36:2671-2680(1998).
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UJN-2001 (TrEMBLrel. 17, Last annotation update)
P28-3 (MAJOR OUTER MEMBRANE PROTEIN P30-4).
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0.00029;
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J. Clin. Microbiol. 36:2671-2680(1998)
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                                                                                                                                          STRAIN-OKLAHOMA;
MEDLINE=21153566; PubMed=11254561;
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SEQUENCE FROM N.A.
MEDLINE-OXLAHOMA,
MEDLINE-OXLAHOMA,
Obsahi N., Rikihisa Y., Unver A.;
                                                                                                                                                                                                                                                                                                                                                                                                                            59 NSTVGVFGLKHDWNGGTISN 78
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Gene 254:245-252(2000).
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Best Local Similarity
Matches 13; Conserv
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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ID Q9F475
AC Q9F475;
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MEDLINE-992157; PubMed=10225842;
MEDLINE-992157; PubMed=10225842;
MCBride J.W., Yu, Xj, Walker D.H.;
"Molecular cloning of the gene for a conserved major immunoreactive 28-kilodalton protein of Ehrlichia canis: a potential serodiagnostic
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MEDLINE-2013107; PubMed-10974556;
MCBride J.W., Yu. X.J., Walker D.H.;
"A conserved, transcriptionally active p28 multigene locus of Gene 254:245-252(2000).
                                                                                                                                                                                                                                                                                                                                              Ehrlichia canis.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
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Bacteria, Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
NCBI_TaxID=944;
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                                  Length 280;
                                                                  Indels
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INTECTPO: IPRO02566; Surface_Ag_msp4.
Pfam: PF01617; Surface_Ag_2: 1.
SEQUENCE 280 AA; 30762 MW; BE284A4B94FE3123 CRC64;
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Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MAJOR OUTER MEMBRANE PROPERIN F30-2.
                                Score 81; DB 2; Le:
Pred. No. 6.8e-05;
2; Mismatches 2;
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STRAIN=OKLAHOMA;
MEDLINE=98371112; PubMed=9705412;
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59 NSTVGVFGLKHDWNGGTISN 78
                                  73.6%;
77.8%;
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                                                                                                     1 NTTTGVFGLKQDWDGATI 18
                                                                                                                       Query Match
Best Local Similarity 65.08
Matches 13; Conservative
                                  Query Match 73.6
Best Local Similarity 77.8
Matches 14; Conservative
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RESULT 11 Q9ADV3

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01-JUN-2001 (TrEMBLrel. 17, Last annotation update) 28 KDA OUTER MEMBRANE PROTEIN (FRAGMENT).
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SEQUENCE FROM N.A.
                                                                                SEQUENCE FROM N.A.
                                                                                              STRAIN-LOUISIANA;
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                                                          NCBI_TaxID=944;
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MEDLINE=98084465; PubMed=9423849;
Ohashi N., Zhi N., Zhang Y., Rikihisa Y.;
Immunodominant major outer membrane proteins of Ehrlichia chaffeensis are encoded by a polymorphic:multigene family.";
Infect. Immun. 66:132-139(1998).
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"Molecular characterization of a 28 kDa surface antigen gene family the tribe Ehrlichiae.";
"Molecular characterization of a 28 kDa surface antigen gene family the tribe Ehrlichiae.";
English Ehrolofs. Res. Commun. 247:636-643(1998).
EMBL; 072291; AAC02938.1; -.
EMBL; AR062761; AAC26718.1; -.
EMBL; PR0015761; AAC26718.1; -.
EMBL; PR0015761; AAC3678.1; -.
EMBL; SEQUENCE 286 AA: 31509 MW; F145A79270F386BE CRC64;
 "Analysis of Transcriptionally Active Gene Clusters of Major Outer
Membrane Protein Multigene Family in Ehrlichia canis and E.
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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
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Pred. No. 0.0026;
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                                                                                                                                                                5; Indels
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                                          EMBL; AF082744; AAC14358.1; -...

EMBL; AF324792; AAK31313.1; -...

EMBL; AF078553; AAK28697.1; -...

Interpro; IPRO5566; Surface_Ag_msp4.

Pfam; PF01617; Surface_Ag_2; 1.

SEQUENCE 276 AA; 30659 MW; CE51AB37D17AF3A4 CRC64;
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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                                  Infect. Immun. 69:2083-2091(2001).
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MEDLINE-98321180; PubMed-9647746;
                                                                                                                                         69.1%;
65.0%;
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66.7%;
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01-JUN-1998 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                          Query Match
Best Local Similarity
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=945;
                        chaffeensis.";
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Q9R8A9;
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STRAIN-OKLAHOMA;
MCBride J.W., Yu X.J., Walker D.H.;
"Molecular cloning of a conserved major immunoreactive 28-kilodalton protein gene from a polymorphic multiple gene family of Ehrlichia
                                                                                                                                                                           MCBride J.W., Yu.X.J., Walker D.H.;
"Molecular cloning of a conserved major immunoreactive 28-kilodalton canis.";

Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.

BMBL, AR08745; AAC64551.;

InterPro; IPR002566; Surface_Ag_msp4.

Pfan; PR01617; Surface_Ag_2; 1.

NON_TER

ST8 A3, 30485 MW; 697CB6CA413BBA68 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 17, Last annotation update)
01-MON-2001 (TrEMBLREL. 17, Last annotation update)
ENDA OUTER MEMBRANE PROTEIN (FRAGMENT).
ENTICHIA canis.
Bacteria, Proceobacteria; alpha subdivision, Rickettsiales;
Rickettsiaceae, Ehrlichieae; Ehrlichia.
Ehrlichia canis.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.6%; Score 70; DB 2; Length 278; 70.6%; Pred. No. 0.0037; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.6%; Score 70; DB 2; Length 278; 70.6%; Pred. No. 0.0037;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30485 MW; 697CB6CA413BBA68 CRC64;
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Best Local Similarity 70.6
Matches 12; Conservative
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Best Local Similarity 70.6
Matches 12; Conservative
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March 14, 2002, 09:09:37 ; Search time 111.55 Seconds
(without alignments)
13.281 Million cell updates/sec
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/SIDSB/gcgdata/geneseg/genesegp/AA1991.DAT:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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1 NTTVGVFGLKQNWDGSAISN 20
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	E. chafeensis p28	Ehrlichia chaffeen	Ehrlichia chaffeen	Variable surface a	Ehrlichia chaffeen	Ehrlichia chaffeen	Major antiqenic pr	E. chafeensis OMP-	Ehrlichia chaffeen	Ehrlichia chaffeen	Variable surface a
	ID	AAY06942	AAW51095	AAB36189	AAU04199	AAW51089	AAB36183	AAU04193	AAY 06943	AAW51094	AAB36188	AAU04198
	DB	20	19	21	22	19	21	22	20	19	21	22
	Query Match Length DB ID	256	276	276	276	280	280	280	281	280	280	280
æ	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	85.0	85.0	85.0
	Score	107	107	107	107	107	107	107	107	91	91	91
	Result No.	1	7	m	4	S	9	7	ω	6	10	11

E. chafeensis OMP- E. canis P30 prote E. canis P30-2 pro Ehrlichia canis im Ehrlichia canis im	E. chafeensis OMP- Ehrlichia chaffeen Variable surface a Ehrlichia cania im	E. canis P30-1 pro E. canis P30-4 pro Variable surface a Fhrichia canis V8	cani	Ehrlichia chaffeen E. chafeensis OMP- Ehrlichia chaffeen	Variable surface a E. chafeensis OMP- Cowdria ruminantiu Cowdria ruminatiu	ntige dium rotei	پيلم پيلم	408	6 C.
AAY06948 AAY06959 AAY06962 AAY71479 AAW51092	AAY06946 AAB36186 AAU04196 AAY71477	AAY06961 AAY06964 AAU04201 AAW51097	AAB36191 AAY71480 AAY71478	AAW51093 AAY06947 AAB36187	AAU04197 AAY06945 AAW51088 AAB36182	AAU04192 AAR75396 AAB93202	AAW49874 AAG26694 AAG28238	AAB74663 AAP70092 AAP71705	AAR84187 AAP70094
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280 280 280 280 280	286 286 286 278	307 276 132 133	133 133 283	278 278 278	278 280 287 287	287 1037 782	956 117 336	576 110 111	111 364
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88 82 80 80 73	73 73 73	72 68 61.5	61.5 61.5 61.5	09	60 60 51	51 44 43.5	4 4 4 2 2 4	424141	41
113 114 115		225 232 24 24	25 26 27		33 33 34	35 36 37	3 3 8 8 9 9 9 9	444	44 45

ALIGNMENTS

RESULT

Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30; detection; dog. AAY06942 ID AAY06942 standard; Protein; 256 AA. 98WO-US19600. (first entry) E. chafeensis p28 protein. Ohashi N, Rikihisa Y; (quis) UNIV OHIO STA Ehrlichia chafeensis. -SU16 WPI; 1999-254290/2 N-PSDB; AAX34742. WO9913720-A1. 18-SEP-1998; 05-JUL-1999 25-MAR-1999 AAY06942; 19-SEP-

Novel outer membrane proteins from Ehrlichia chaffeensis and Ehrlichia canis

Claim 18; Fig 1; 55pp; English.

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           The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafebensis and E. canis. The E. chafebensis proteins form part of the OMP family and consist of proteins OMP-1. -1(B to Z) shown in AAVG643-982 The E. canis proteins form part of the P30 family and consist of proteins shown in AAVG659-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is the near full-length variable surface antigen VSA5 protein of Ehrlichia chaffeensis; it lacks about 5-7 C-terminal amino acid residues.

The VSA5 amino acid sequence was deduced from a partial open reading frame (ORF5) of a genomic locus (see AAV07179) of E. Chaffeensis that was obtained on the basis of homology to the major antigenic protein MAPI (see AAW51088) of Cowdria ruminantium. This genomic locus included 5 ORFs encoding similar, but non-identical scene AAW51091-95). A claimed composition comprises a nucleic acid (see AAW51082) encoding a polypeptide (see AAW510899) that elicits a protective immune response against a rickettaial pathogen. The nucleic acid is used, in human or veterinary medicine, in vaccines to protect against Rickettsia, Ehrlichia,
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Composition containing nucleic acid encoding rickettsial antigen - useful for, e.g. stimulating protective immune response in humans or
                                                                                                                                                                                                           ö
                                                                                                                                                                           Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAP1 homologue; variable surface antigen; VSA5; rickettsia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McGuire TC;
                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ehrlichia chaffeensis VSA5 protein (partial seguence).
                                                                                                                                                                           Score 107; DB 20;
Pred. No. 2.5e-09;
Mismatches 0;

    1..25
    /note= "putative signal peptide"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ganta RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                       AAW51095 standard; Protein; 276 AA.
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0
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                                                                                                                                                                           100.08;
ilarity 100.08;
Conservative 0,
                                                                                                                                                                                                                                         1 NTTVGVFGLKQNWDGSAISN 20
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                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barbet AF, Burridge MJ,
Nyika A, Rurangirwa FR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UYFL ) UNIV FLORIDA
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N-PSDB; AAV07179.
                                                                                                                                                                           Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                           256 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA vaccine
                                                                                                                                                                                                                                                                                                                                                                                      AAW51095;
                                                                                                                              Sequence
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AAW51095
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The present sequence shows a high degree of similarity to the major antigenic protein 1 (MAPI) of Ehrlichia sp. The MAPI gene may be used in a vaccines to protect animals or humans against rickettsial diseases caused by a organisms of Rickettsia sp., Ehrlichia sp., Anaplasma sp. or Cowdria sp. The vaccine elicits an immuse response protective against the rickettsial pathogen. The nucleic acid vaccines can be driven by the human cytomegalovirus (HGWV) enhancer-promoter. Cowdria ruminatium genes designated map 2, Ihworf3, 4hworf1, 18hworf1 and 3gdorf3 may be used in therapeutic and diagnostic applications. The polypeptides are useful for detecting antibodies associated with infection by a rickettsial pathogen whilst the polynucleotides may be used to detect the presence of rickettsial nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides useful as DNA vaccines for conferring immunity to rickettsial infection e.g. heartwater caused by Cowdria ruminantium, comprises major antigenic protein 1 or 2 gene of rickettsial pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ganta RR, Burridge MJ, Mahan SM, McGuire TC; d AL, Simbi BH, Whitmire WW, Alleman AR;
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ehrlichia chaffeensis; VSA5; variable surface antigen 5; MAP1; and or antigence protein 1; antirickettsial; vaccine; gene therapy; Rickettsia; Cowdria; Anaplasma; map2; Ihworf3; 4hworf1; 18hworf1; Rickettsia; Cowdrae; Anaplasma; map2; Anaprisma; Anaprisma; Anaplasma; Map2; Anaprisma; Anaprisma; Map2; Anaprisma; Anaprisma; Map2; Anaprisma; Anaplasma; Map2; Anaprisma; Anaprisma; Map2; Anaprisma; Anaprisma; Map2; Anaprisma; Anaprisma; Map2; Anaprisma; Anaprisma; Map2; 
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                                                                                                                                                                                                                    Length 276;
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Anaplasma and Cowdria species. The Bhrlichia antigenic bolypeptides can be used diagnostically to detect antibodies associated with Bhrlichia infection (claimed).
                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                Score 107; DB 19;
Pred. No. 2.7e-09;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB36189 standard; Protein; 276 AA.
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                                                                                                                                                                                                             Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 20; Conservative 0
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                                                                                                                                                                                                                                                                                                                                           1 NTTVGVFGLKQNWDGSAISN 20
                                                                                                                                                                                                                                                                                                                                                                           59 nttvgvfglkgnwdgsaisn 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYFL ) UNIV FLORIDA.
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N-PSDB; AAC68706.
                                                                                                                      276 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barbet AF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB36189;
                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3gdorf3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
AAB36189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.5005
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AAU04199;

AAU04199

59

Matches

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Ehrlichia chaffeensis; MAPI; major antigenic protein 1; antirickettsial; vaccine; gene therapy; Rickettsia; Cowdria; Anaplasma; map2; 1hworf3; 4hworf1; 18hworf1; 3gdorf3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composition containing nucleic acid encoding rickettsial antigen - useful for, e.g. stimulating protective immune response in humans or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This polypeptide comprises the major antigen protein I gene (MAPI) of Ehrlichia chaffeensis. It is encoded by the MAPI gene (see AAV07177).

A claimed composition comprises a nucleic acid (see PAV07176-82) encoding a polypeptide (see AAW31088-99) that elicits a protective immune response against a rickettsial pathogen. The nucleic acid is used, in human or veterinary medicine, in vaccines to protect against Rickettsia. Bhriichia, Anaplasma and Cowdria species. The nucleic acid does not replicate in the host but remains episomal and capable of expressing polypeptide for at least 19 mth. The Ehrlichia antigenic polypeptides can be used diagnostically to detect antibodies associated with Ehrlichia
                                                                                                                                                                                             MAP1 gene; major antigénic protein 1; rickettsia; DNA vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mahan SM, McGuire TC;
                                                                                                                                                        Ehrlichia chaffeensis major antigenic protein 1 (MAP1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 107; DB 19;
Pred. No. 2.7e-09;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ganta RR,
                                      AAW51089 standard; Protein; 280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 18-19; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB36183 standard; Protein; 280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
ilarity 100.0%;
Conservative 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NTTVGVFGLKQNWDGSAISN 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96US-0733230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ehrlichia chaffeensis MAP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burridge MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nyika A, Rurangirwa FR;
                                                                                                                                                                                                                                   Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                (UYFL ) UNIV FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .nfection (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-251232/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAV07177
                                                                                                                                                                                                                                                                        WO9816554-A1.
                                                                                                                                                                                                                                                                                                                                                   17-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                          17-OCT-1996;
                                                                                                                 14-SEP-1998
                                                                                                                                                                                                                                                                                                              23-APR-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB36183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barbet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB36183
                AAW51089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence represents the amino acid sequence of variable surface antigen 5 (VSA5) isolated from Ehrlichia chaffeensis, which has similarity to major antigen protein (MAP). The MAP polynucleotides and polypeptides are useful as vaccines for conferring immunity to rickettsia infection, including Cowdria ruminantium causing heartwater. The MAP polynucleotides may be used as molecular markers in nucleic acid analysis procedures, and to produce the MAP polypeptides, which may be used to raise antibodies that are reactive with the polypeptides. The nucleic acids may further be used as probes to identify complementary sequences within other nucleic acid molecules or genomes, where such probes can be applied to identify or distinguish infectious strains of organisms in diagnostic procedures or in rickettsial research where identification of particular organisms or strains is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New MAP2 genes and polypeptides useful as vaccines for conferring immunity to human and animal rickettsial diseases, e.g. heartwater, or as molecular markers in nucleic acid analysis procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                     Major antigenic protein; MAP; vaccine; immunogenic; rickettsia; infection; heartwater; diagnostic; variable surface antigen; VSA.
                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                               Variable surface antigen 5 (VSA5) from Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nyika A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 107; DB 22;
100.0%; Pred. No. 2.7e-09;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McGuire TC, Burridge MJ,
SM, Bowie MV, Alleman AR;
                                      ö
                  Pred. No. 2.7e-09;
                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Fig 2A-2B; 30pp; English.
                                                                                                                                                                                                             AAU04199 standard; Protein; 276 AA.
100.0%; FL
0;
                                                                                             1 NTTVGVFGLKQNWDGSAISN 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NTTVGVFGLKQNWDGSAISN 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0733230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0953326
                                                                                                                                                                                                                                                                                        23-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barbet AF, Ganta RR,
Rurangirwa FR, Mahan
                                                                                                                                                                                                                                                                                                                                                                                                                            Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYFL ) UNIV FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-424487/45.
                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  276 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAS07578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-0CT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US6251872-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-OCT-1996;
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Indels

Sequence

Query Match

59

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Length 280;

or

Nyika A;

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The sequence represents the amino acid sequence of major antigenic protein i (MAPI) from Ehrlichia chaffeensis. The MAP polynucleotides and polyapetides are useful as vaccines for conferring immunity to rickettsia infection, including Cowdria ruminantium causing heartwater. The MAP polynucleotides may be used as molecular markers in nucleic acid analysis procedures, and to produce the MAP polyapetides, which may be used to raise antibodies that are reactive with the polypeptides. The nucleic acids may further be used as probes to identify complementary sequences within other nucleic acid molecules or genomes, where such probes can be applied to identify or distinguish infectious strains of organisms in diagnostic procedures or in rickettsial research where identification of particular organisms or strains is
                                                                                                                                                                                                    New MAP2 genes and polypeptides useful as vaccines for conferring immunity to human and animal rickettsial diseases, e.g. heartwater, as molecular markers in nucleic acid analysis procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel outer membrane proteins from Ehrlichia chaffeensis and
                                                                                 Burridge MJ,
Alleman AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 107; DB 22;
Best Local Similarity 100.0%; Pred, No. 2.7e-09;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                     Disclosure; Column 15-17; 30pp; English.
                                                                                 McGuire TC, Bo
M, Bowie MV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY06943 standard; Protein; 281 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 NTTVGVFGLKQNWDGSAISN 20
96US-0733230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E. chafeensis OMP-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-US19600.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0059353.
                                                                                                    SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 nttvgvfglkqnwdgsaisn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (OHIS ) UNIV OHIO STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohashi N, Rikihisa Y;
                                                                               Ganta RR,
'R, Mahan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ehrlichia chafeensis.
                                      (UYFL ) UNIV FLORIDA
                                                                                                                                             WPI; 2001-424487/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-254290/21.
N-PSDB; AAX34743.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 AA;
                                                                                                                                                                N-PSDB; AAS07576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detection; dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09913720-A1.
17-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-1999
                                                                                 Barbet AF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY06943;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  needed.
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g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is given in a specification relating to nucleic acid vaccines containing genes to protect animals or humans against rickettsial diseases caused by a organisms of Rickettsia sp., Ehrlichia sp., Amaplasma sp. or Cowdria sp. The vaccine elicits an immune response protective against the rickettsial pathogen. The vaccine comprises the major antigenic protein 1 (MAP2) gene or the major antigenic protein 2 (MAP2) gene or the major antigenic protein 2 (MAP2) gene or the major antigenic protein 3 (MAP2) gene or the major antigenic protein 3 pathogens. The nucleic acid vaccines can be runninatium genes designated map 2, lhworfl, shworfl, 18hworfl and 3gdorf3 may be used in therapeutic and diagnostic applications. The polypoptides are useful for detecting antibodies associated with infection by a rickettsial pathogen whilst the polypucleotides may be used to detect the presence of rickettsial nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotides useful as DNA vaccines for conferring immunity to rickettsial infection e.g. heartwater caused by Cowdria ruminantium, comprises major antigenic protein 1 or 2 gene of rickettsial pathogens
                                                                                                                                                                                                                                                                     TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                Barbet AF, Bowie MV, Ganta RR, Burridge MJ, Mahan SM, McGuire Rurangirwa FR, Moreland AL, Simbi BH, Whitmire WW, Alleman AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Major antigenic protein 1; MAP1; vaccine; immunogenic; rickettsia; infection; heartwater; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Major antigenic protein 1 (MAP1) from Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 107; DB 21;
Pred. No. 2.7e-09;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 35-36; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU04193 standard; Protein; 280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; P
Matches 20; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-APR-2000; 2000WO-US10886
                                                                                                                                                                                 99US-0130725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                   Ehrlichia chaffeensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ehrlichia chaffeensis
                                                                                                                                                                                                                         (UYFL ) UNIV FLORIDA.
                                                                                                                                                                                                                                                                                                                            WPI; 2000-679675/66.
N-PSDB; AAC68700.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 AA;
                                                           WO200065063-A2
                                                                                                                                                                                 22-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-OCT-2001
                                                                                                  02-NOV-2000
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Gaps

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Indels

Length 280;

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rickettsial pathogen. The nucleic acid is used, in human or veterinary medicine, in vaccines to protect against Rickettsia, Ehrlichia, Anaplasma and Cowdria species. The Ehrlichia antigenic polypeptides can be used diagnostically to detect antibodies associated with Ehrlichia infection (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                  88888888
                                                                                                                                                                                                                                               Db
                                                                                                                                                                                                                  δy
                                                                                                                                                                                                                                                                ÷
                                                             The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in AAY06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAY06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ehrlichia chaffeensis. Its amino acid sequence was deduced from a partial open reading frame (ORF4) of a genomic locus (see AAV07179) of E. chaffeensis that was obtained on the basis of homology to the major antigenic protein MAPI (see AAW51088) of Cowdria ruminantium. This genomic locus included 5 ORFs encoding similar, but mon-identical proteins (see AAW51091-95). A claimed composition comprises a nucleic acid (see AAV07105-82) encoding a polypeptide (see AAW51088-99) that elicits a protective immune response against a
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Composition containing nucleic acid encoding rickettsial antigen - useful for, e.g. stimulating protective immune response in humans or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the full-length variable surface antigen VSA4 protein of
                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                             Length 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homologue; variable surface antigen; VSA4; rickettsia;
                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McGuire
                                                                                                                                                                                                                               100.0%; Score 107; DB 20; 100.0%; Pred. No. 2.8e-09;
                                                                                                                                                                                                                                                                ;
0
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/note= "putative signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mahan SM,
                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ehrlichia chaffeensis VSA4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                             AAW51094 standard; Protein; 280 AA
                                  Disclosure; Fig 3B; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ganta
                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                             1 NTTVGVFGLKQNWDGSAISN 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-US19044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-0733230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burridge MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nyika A, Rurangirwa FR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYFL ) UNIV FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-251232/22.
N-PSDB; AAV07179.
                                                                                                                                                                                                                                                Sest Local Similarity
                                                                                                                                                                               281 AA;
 Ehrlichia canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-0CT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-0CT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9816554-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-APR-1998,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA vaccine
                                                                                                                                                                                                                                                                20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barbet AF,
                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
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                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                               59
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diseases caused by a organisms of Rickettsia sp., Ehrlichia sp., Anaplasma sp. or Cowdria sp. The vaccine elicits an immune response protective against the rickettsial pathogen. The nucleic acid vaccines can be driven by the human cytomegalovirus (HCWV) enhancer-promoter. Cowdria ruminatium genes designated map 2, 1hworf3, 4hworf1, 18hworf1 and 3gdorf3 may be used in therapeutic and diagnostic applications. The polypeptides are useful for detecting antibodies associated with infection by a rickettsial pathogen whilst the polynucleotides may be used to detect the presence of rickettsial nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotides useful as DNA vaccines for conferring immunity to rickettsial infection e.g. heartwater caused by Cowdria ruminantium, comprises major antigenic protein 1 or 2 gene of rickettsial pathogens
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence shows a high degree of similarity to the major antigenic protein 1 (MAP1) of Ehrlichia sp. The MAP1 gene may be used in a vaccines to protect animals or humans against rickettsial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SM, McGuire
Alleman AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   major antigenic protein 1; antirickettsial; vaccine; gene therapy;
Rickettsia; Cowdria; Anaplasma; map2; lhworf3; 4hworf1; 18hworf1;
                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ehrlichia chaffeensis; VSA4; variable surface antigen 4; MAP1;
                                                                              Length 280;
                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bowie MV, Ganta RR, Burridge MJ, Mahan PR, Moreland AL, Simbl BH, Whitmire WW,
                                                                                 Score 91; DB 19;
Pred. No. 1e-06;
                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ehrlichia chaffeensis partial VSA4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 45-46; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         AA.
                                                                                                                                                                                                                                                                                                                                                                                                      AAB36188 standard; Protein; 280
                                                                                                                                       2;
                                                                                    85.0%;
84.2%;
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                                                                                                                                                                                                   NTTVGVFGLKQNWDGSAIS 19
                                                                                                                                                                                                                                 99US-0130725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ehrlichia chaffeensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYFL ) UNIV FLORIDA
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N-PSDB; AAC68705.
                                                                                 Query Match
Best Local Similarity
Matches 16; Conserv
AA:
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   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB36188;
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Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30; detection; dog.
 RESULT 12
AAX06948
ID AAY06948 standard; Protein; 280 AA.
                                                                                                E. chafeensis OMP-1F protein.
                                                                                                                                                                                                                                                                          (OHIS ) UNIV OHIO STATE.
                                                                                                                                                                                                                                                                                                 Ohashi N, Rikihisa Y;
                                                                                                                                                         Ehrlichia chafeensis.
                                                                                                                                                                                WO9913720-A1.
                                                                                                                                                                                                                            18-SEP-1998;
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                                                                         05-JUL-1999
                                                                                                                                                                                                       25-MAR-1999.
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                           ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence represents the amino acid sequence of variable surface has similarity to major antigen protein (MAP). The MAP polynuclectides and polypeptides are useful as vaccines for conferring immunity to rickettsia infection, including Cowdia runnantium causing heartwater. The MAP polynucleotides may be used as molecular markers in nucleic acid manaysis procedures, and to produce the MAP polypeptides, which may be used to raise antibodies that are reactive with the polypeptides. The nucleic acids may further be used as probes to identify complementary sequences within other nucleic acid molecules or genomes, where such probes can be applied to identify or distinguish infectious strains of organisms in diagnostic procedures or in rickettsial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New MAP2 genes and polypeptides useful as vaccines for conferring mimunity to human and animal ricketrsial diseases. e.g. heartwater, as molecular markers in nucleic acid analysis procedures
                                                                                                                                                                                                                            Major antigenic protein; MAP; vaccine; immunogenic; rickettsia; infection; heartwater; diagnostic; variable surface antigen; VSA
                           .
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                                                                                                                                                                                                     Variable surface antigen 4 (VSA4) from Ehrlichia chaffeensis.
Score 91; DB 21; Length 280;
Pred. No. 1e-06;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Nyika A;
                                                                                                                                                                                                                                                                                                                                                                                                    Barbet AF, Ganta RR, McGuire TC, Burridge MJ, Rurangirwa FR, Mahan SM, Bowie MV, Alleman AR;
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                                                                                                                                 AAU04198 standard; Protein; 280 AA.
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                                                                                                                                                                                                                                                                                                                                                        96US-0733230.
                                               (first entry)
 Query Match 85.0
Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                                                                                             Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                               (UYFL ) UNIV FLORIDA
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N-PSDB; AAS07578.
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                                                                                                                                                                                                                                                                                                                               17-OCT-1997;
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                                                                                                                                                                              23-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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98WO-US19600. 97US-0059353.

(first entry)

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                                                                                                                                                       The invention provides isolated outer membrane proteins (OMP) from brilionia chafeensis and E. Canis. The E. Chaffegenis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to 2) shown in AAVO6943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAVO6959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30; detection; dog.
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                                                           Novel outer membrane proteins from Ehrlichia chaffeensis and Ehrlichia canis
                                                                                                                                                                                                                                                                                                                                                                 Length 280;
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                                                                                                                                                                                                                                                                                                                                                                 Score 88; DB 20; I
Pred. No. 3.1e-06;
L; Mismatches 2;
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                                                                                                                       Claim 16; Fig 8B; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                 82.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NTTVGVFGLKONWDGSAIS 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 ntttgvfglkqdwdgstis
WPI; 1999-254290/21.
N-PSDB; AAX34748.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E. canis P30 protein.
                                                                                                                                                                                                                                                                                                        280 AA;
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                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                    Query Match
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AAY0699
TO AAY0699
XX AAY0695
XX AAY0695
XX XX AAY0695
XX AAY0699
DT 05-JUL-
XX XX AAY0699
XX AAY0699
XX AAY099137
XX XX AAY099137
XX XX AAY099137
XX XX XX AAY099137
XX XX XX AAY099137
XX XX XX AAY099137
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Gaps

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Score 91; DB 22; Length 280; Pred. No. 1e-06; 2; Mismatches 1; Indels

5;

Ouery Match 85.0%; Best Local Similarity 84.2%; Matches 16; Conservative ;

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WPI; 2000-412298/35
                                                                          Best Local Similarity
Matches 14; Conserv
                                         280 AA;
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                                                                                                                                                                                                                                                                                                                                                                           24-NOV-1999;
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                                                                                                                                                                                              12-0CT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Walker DH,
                                                                                                                                                                                                                                                                        Ehrlichia
                                                                                                                                                                             AAY71479;
                                          Sequence
                                                                   Query Match
                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                          Key
                                                                                                                                             RESULT
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                                                                                                                                          The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, ^{-1}(B to Z) shown in AAV06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAV06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and E. canis. The E. chaffeensis proteins form part
                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                          Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30;
                                                                                                                                                                                                                                               .
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                                                                                                  Novel outer membrane proteins from Ehrlichia chaffeensis and Ehrlichia canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 outer membrane proteins from Ehrlichia chaffeensis and
                                                                                                                                                                                                                              DB 20; Length 288; 3e-05;
                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                              Score 82;
Pred. No.
                                                                                                                                                                                                                                                                                                                         AAY06962 standard; Protein; 280 AA.
                                                                                                                          Disclosure; Fig 19B; 55pp; English.
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                                                                                                                                                                                                                                                                       76.6%;
70.0%;
                                                                                                                                                                                                                                                               1 NTTVGVFGLKQNWDGSAISN 20
       98WO-US19600.
                       97US-0059353
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                                                                                                                                                                                                                                                                                                                                                          05-JUL-1999 (first entry)
                                                                                                                                                                                                                        Query Match
Best Local Similarity 70.09
                                       (OHIS ) UNIV OHIO STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (OHIS ) UNIV OHIO STATE
                                                                                                                                                                                                                                                                                                                                                                           E. canis P30-2 protein
                                                        Ohashi N, Rikihisa Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohashi N, Rikihisa Y;
                                                                       WPI; 1999-254290/21.
N-PSDB; AAX34759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-254290/21
                                                                                                                                                                                                     288 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAX34762
                                                                                                                                                                                                                                                                                                                                                                                                                   Ehrlichia canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ehrlichia canis
                                                                                                                                                                                                                                                                                                                                                                                                     detection; dog
                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9913720-A1
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       18-SEP-1998;
                       19-SEP-1997;
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of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in AAYO6943-98B. The E. canis proteins form part of the P30 family and consist of proteins shown in AAYO6959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homologous 28-kDa protein gene; ECa28SA3; immunoreactive; vaccine; p28 gene; p0.0 ymorphic multiple gene family; immunoprotective antigen; antibacterial; canine ehrlichiosis; canine tropical pancytopaenia; tick-borne rickettsial disease; serodiagnosis.
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                                                                                                                                                                                                                                                                                                DB 20; Length 280;
                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Mature_ECa28SA3_28-kDa_protein
                                                                                                                                                                                                                                                                                                                                                                     3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ehrlichia canis immunoreactive protein ECa28SA3.
                                                                                                                                                                                                                                                                                                                                   6e-05;
                                                                                                                                                                                                                                                                                                                                      Pred. No. 6e-C
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY71479 standard; Protein; 280 AA.
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CC mature 28-kDa protein by cleavage of N-terminal signal sequence. XX Sequence 280 AA;
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Search completed: March 14, 2002, 09:09:37 Job time: 428 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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MEDLINE-98321180; Pubwed-9647746;
MEDLINE-98321180; Pubwed-9647746;
MEDGR. Sulsona C.R., Barbet A.F., Mahan S.M., Burridge M.J.,
Alleman A.R.;
"Molecular characterization of a 28 kDa surface antigen gene family of the tribe Ehrlichiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-ARKANSAS;
MEDLINE-98084465; PubMed-9423849;
Ohashi N., Zhi N., Zhang Y., Rikihisa Y.;
Immunodominant major guter membrane proteins of Ehrlichia chaffeensis
are encoded by a polymorphic multigene family.";
Infect. Tmmun. 66:132-139(-1998).
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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Ehrlichieae; Ehrlichia.

NCBI_TaxID=945;
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052104;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-2001 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
00P-1C (28 KDA MAJOR SURFACE ANTIGEN-1).
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EMBL; U72291; AAC02937.1; -
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Best Local Similarity 100.
Matches 18; Conservative
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1 NPTVALYGLKQDWNGVSA 18

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STRAIN-OKLAHOMA;

BDLINE-21153566; PubMed-11254561;

Chashi N., Rikihisa Y., Unver A.;

"Analysis of Transcriptionally Active Gene Clusters of Major Outer

Membrane Protein Multigene Family in Ehrlichia canis and E.

chaffeensis.";

co. nora-2001(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P30-2.
Bhrlichia canis.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
NCBI_faxID=944;
SEQUENCE FROM N.A.
STAIN-JARE,
MEDLINE-20432107; PubMed-10974556;
MCBLINE-20432107; PubMed-10974556;
MCBLINE-20432107; PubMed-10974556;
MCBLICONS TOWER, TOWER D.H.;
"A consorved, transcriptionally active p28 multigene locus ehrlichia canis.";
EMPL: A46-252(200).
EMBL: AF082744; AAG14361.1; -.
EMBL: AF082744; AAG14361.1; -.
PITATEPTO: IPRO02566; Surface_A9_msp4.
PFORE TOWER TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=OKLAHOMA;
MEDLINE-198371112; PubMed-9705412;
Ohashi N., Unver A., Zhi N., Rikihisa Y.;
Cloning and characterization of multigenes encoding the immunodominant 30-kilodalton major outer membrane proteins elmlichia canis and application of the recombinant protein serodiagnosis."
                                                                                                                                                                                                                                                                                                                                                                    Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 280;
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EMBL, AF078553, AAK28699.1, -.
SEQUENCE 280 AA; 30803 MW; 27238BEIC7E68A91 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN P30-2.
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Pred. No. 0.032;
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Best Local Similarity 66.7%;
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085357, 085367,
015087,
01-NOV-1998 (TrEMBLECL: 08,
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59 NSTVGVFGLKHDWNG 73
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MEDLINE-BRAZINES;
MEDLINE-BRAZINES;
Reddy G.R., Sulsona C.R., Barbet A.F., Mahan S.M., Burridge M.J.,
Alleman A.R.;
Molecular characterization of a 28 kDa surface antigen gene family of
the tribe Ehrlichiae.";
Hiochan Biophys. Res. Commun. 247:636-643(1998).
EMBL: 072291; AAC26719.1: -.
EMBL: AF062761; AAC26719.1: -.
FEMBL: PROJECT Surface—Ag_msp4.
Prima: PF01617; Surface—Ag_msp4.
SEQUENCE 278 AA; 30543 MW; E321E3CA259B87FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECUENCE FROM N.A.
STRAIR-ARKANSAS;
MEDLINE=98084465; Pubwed=9423849;
Ohashi N., Zhi N., Zhang Y., Rikihisa Y.;
"Immunodominant major outer membrane proteins of Ehrlichia chaffeensis are encoded by a polymorphic multigene family.";
infect. Immun. 66:132-139(1998).
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=99242757; Pubwed=10225842;
MEDLINE=99242757; Pubwed=10225842;
MCBLINE=1001ing of the gene for a conserved major immunoreactive "Molecular cloning of the gene for a conserved major immunoreactive 28-kilodalton protein of Ehrlichia canis: a potential serodiagnostic.
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Rickettsiaceae; Ehrlichieae; Ehrlichia.
NCBI_TaxID=945;
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Bacteria: Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae: Ehrlichieae; Ehrlichia.
NCBI_TaxID=944;
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09F473;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
P28-6
                                                                                                                                                                                                                          01.JUN-1998 (TrEMBLrel. 06, Created)
01.JUN-1998 (TrEMBLrel. 06, Last sequence update)
01.JUN-1998 (TrEMBLrel. 17, Last annotation update)
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[2]
                                                                                                                                                                          PRT;
      60 NPTVALYGLKQDWNGVSA 77
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Best Local Similarity
Matches 15; Conserv
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Yu.X.J., McBride J.W., Walker D.H.;

"Genetic diversity of the 28-kilodalton outer membrane protein gene in human isolates of Ehrlichia chaffeensis.";
J. Clin. Microbiol. 37:113-1143(1999).

EMBL, AF077735, AAC31548.1;

Enterpro; IPR001702; Gram_neg_porin.

InterPro; IPR002565, Surface_Ag_msp4.

Pfam; PF01617; Surface_Ag_2: 1.
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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
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Bacteria, Proteobacteria, alpha subdivision, Rickettsiales,
                                                                                                                         Length 288;
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"Ehrlichia chaffeensis 28 kDa outer membrane protein.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AR077734; AAC31547.1; -.
InterPro; IPRO556; Surface_Ag_msp4.
Fign; PF01617; Surface_Ag_2; 1.
SEQUENCE 276 AA; 30027 MW; ZFD3698FCF1F60BE CRC64;
      17; Surface_Ag_2; 1.
288 AA; 31590 MW; 86DCAECB88E9BF5E CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
00TER MEMBRANE PROTEIN P28 PRECURSOR (FRAGMENT).
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
OUTER MEMBRANE PROTEIN P28 PRECURSOR.
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                                                                                                                         Score 59; DB 2;
Pred. No. 0.1;
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NCBI_TaxID=945;
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STRAIN=ST.VINCENT;
MEDLINE=99175287; PubMed=10074538;
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PRINTS; PR00182; ECOLNEIPORIN.
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SEQUENCE 246 AA; 26884 MW;
                                                                                                                         60.2%;
52.9%;
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60 NTTTGVFGLKQDWDGAT 76
                                                                                                                                                     Best Local Similarity 52.9
Matches 9; Conservative
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Best Local Similarity 60.0
Matches 9; Conservative
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29 NTTAGVFGLKQDWDG 43
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         Pfam; PF01617;
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                                     SEQUENCE
                                                                                                                               Query Match
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Q9RH35;
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                                                                                                                                                                                                                                                                                                                                                         "Molecular characterization of a 28 kDa surface antigen gene family of the tribe Enrilofiae.";
Blochem. Blophys. Res. "0.
Blochem. Biophys. Res. "1.
EMBL, AF062761; AAC26720.1; "1.
InterPro: IPRO02566; Surface—Ag_msp4.
Pfam: PF01617; Surface—Ag_2: 1.
SEQUENCE 280 AA: 30743 MW; FBB841DAF08EE4DC CRC64;
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BEDLINE-19821180; PubMed-9647746;
Reddy G.R., Sulsona C.R., Barbet A.F., Mahan S.M., Burridge M.J.,
Alleman A.R.;
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MEDLINE=98371112; PubMed=9705412;
Ohashi N., Unver A., Zhi N., Rikihisa Y.;
"Cloning and characterization of multigenes encoding the immunodominant 30-kilodalton major outer membrane proteins of Ehrlichia canis and application of the recombinant protein for serodiagnosis.";
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McBride J.W., Yu X.J., Walker D.H.;
"A conserved, transcriptionally active p28 multigene locus of
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
28 KDA MAJOR SURFACE ANTIGEN-4.
Ehrlichia chaffeensis.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
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Bacteria: alpha subdivision; Rickettsiales; Rickettsiaceae; Ehrlichieae; Ehrlichia.
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Pred. No. 0.046;
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
30-KDA MAJOR OUTER MEMBRANE PROTEIN (P28-8).
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Gene 254:245-252(2000).
EMBL, AF078553, AAC68667.1; -.
EMBL, AR078553, AAC6865.1; -.
InterPro; IPR002566; Surface_Ag_msp4.
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60.0%;
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60 NTTIGVFGLKQDWDG 74
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                     NCBI_TaxID=945
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STRAIN-ARKANSAS;
MEDLINE-980844465; PubMed-9423849;
Ohashi N., Zhi N., Zhang Y., Rikihisa Y.;
Immunodominant major outer membrane proteins of Ehrlichia chaffeensis
are encoded by a polymorphic multigene family.";
infect. Immun. 66:132-139(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=ARKANSAS;
MDDLINE-21153566; PubMed-11254561;
Ohashi N., RikLhisa Y., Unver A.;
Ohashi N., RikLhisa Y., Unver A.;
MAnalysis of Transcriptionally Active Gene Clusters of Major Outer
Membrane Protein Multigene Family in Ehrlichia canis and E.
chaffeensis.";
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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Cowdria.
NCBL_TaxID=15.2574;
                                                                                                                                                                                                                                                                                                                                           Ehrlichia chaffeensis.
Bacteria, Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
NCBI_TaxID=945;
    Length 276;
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                                         2; Indels
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"A novel Ehrlichia detected in dogs in South Africa.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF325176; AAK14320.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTECEL. IMMIN. 69:2083-2091(2001).
EMBL: U72291; AAK28673.1; -.
SEQUENCE 281 AA; 30343 MW; A99E5F7C4459AA9A CRC64;
                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MAJOR OUTER MEMBRANE PROFEIN P28.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MAJOR ANTIGENIC PROTEIN MAP1 (FRAGMENT).
    Score 57; DB 2;
Pred. No. 0.21;
1; Mismatches
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    58.2%;
60.0%;
    Query Match 58.2
Best Local Similarity 60.0
Matches 9; Conservative
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                                                                               1 NPTVALYGLKQDWNG 15
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59 NTTVGVFGLKQNWDG 73
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59 NTTVGVFGLKQNWDG 73
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Best Local Similarity
Matches 9; Conserv
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Q9ACI9;
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Q9ACI9
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-98084465; PubMed-9423849;
Ohashi N., Zhang Y., Rikihisa Y.;
Ohashi N., Zhang Y., Rikihisa Y.;
Immunodominant major outer membrane proteins of Ehrlichia chaffeensis are encoded by a polymorphic multigene family.";
EMBL: 072291; AAC02940.1:
EMBL: 072291; AAC02940.1:
Infectror, Irmanon 66:132-139(1998).
Fami: PFO1617; Surface_Ag_msp4.
Ffam: PFO1617; Surface_Ag_msp7.
SEQUENCE 280 AA; 30731 MW; CCAA6G34E2AF393E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular characterization of a 28 kDa surface antigen gene family of the tribe Bhrilchiae.";
Biochem. Biophys. Res. Commun. 247:636-643(1998).
EMBL; AF062761, AAC26716.1;
InterPro; IPR002566; Surface_Ag_msp4.
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STRAIN=ARRANSAS;
MEDLINE=98321180; PubMed=9647746;
Reddy G.R., Sulsona C.R., Barbet A.F., Mahan S.M., Burridge M.J.,
Alleman A.R.,
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Bacteria: Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 17, Last annotation update)
28 KDA MAJOR SURFACE ANTIGEN-5 (FRAGMENT).
Ehrlichia chaffeensis.
Ehrlichia chaffeensis.
Rickettslaceae; Ehrlichieae; Ehrlichia.
NCBI_TaxID=945;
Score 58; DB 2; Length 276; Pred. No. 0.14; 3; Mismatches 3; Indels
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  59.2%;
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                                                                             1 NPTVALYGLKODWNG 15
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59 NTTAGVFGLKQDWDG 73
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Bensaid A., Maillard J.-C., Chantal I., Perez J.-M., Martinez D.;
"Cowdria rundiantium major antigenic protein 1 (map1) gene variants
are not geographically constrained.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AFS55200; AAK27216.1;
SEQUENCE 284 AA; 30720 MW; BODJAEB9F9AB09C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                STRAIN-SENEGAL STOCK;
MEDLINE-94178956; PubMed-8132352;
Wan Vliet A.H., Jongejan F., van Kleef M., Van der Zeijst B.A.;
"Molecular cloning, sequence analysis, and expression of the gene encoding the immunodominant 32-Kilodalton protein of Cowdria ruminantium.";
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Rickettsiaceae; Ehrlichieae; Cowdria.
NCBL_TaxID=779;
                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Ehrlichieae; Cowdria.
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                                                                Score 55; DB 2; Length 272;
Pred. No. 0.43;
4; Mismatches 1; Indels
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272 272
272 AA; 29225 MW; 43CEB95DEDD55BDE CRC64;
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EMBL: X74250; CAA53309.1; -
InterPro; IPRO02566; Surface_Ag_msp4.

Pfam; PF01617; Surface_Ag_2: 1.

SEQUENCE 284 AA; 30634 MW; 53228A889928BEB8 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MAJOR ANTIGENIC PROTEIN 1.
                                                                                                                                                                                                                       Q46327;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MAJOR ANTIGENIC PROTEIN.
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Best Local Similarity 64.3%;
Matches 9; Conservative
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57 TKAVFGLKKDWDGV 70
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63 TKAVFGLKKDWDGV 76
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Rickettslaceae; Ehrlichieae; Ehrlichia.
  DB 2; Length 284;
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                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yu X.-J., Walker D.H.;
"Ehrlichia chaffeensis 28 kDa outer membrane protein.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AR07732; ARC31545.1;
InterPro: IPR00256; Surface_Ag_msp4.
Pfan; PF01617; Surface_Ag_2; 1.
SEQUENCE 280 AA; 30277 MW; 91C54AC78507A63F CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-UNV-2001 (TrEMBLrel. 17, Last annotation update)
01-UNV-8001 (TrEMBLRel. 17, Last annotation update)
Score 55; DB 2;
Pred. No. 0.45;
4; Mismatches
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  56.1%;
Query Match 56.1
Best Local Similarity 64.3
Matches 9; Conservative
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61 TAGVFGLKQDWDG 73
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

US-09-765-739A-4 98 1 NPTVALYGLKQDWNGVSA 18 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		Description	Z my	P11637 neurospora	P47024 saccharomyc	Q99626 homo sapien	P55019 pseudopleur							-	Q07307 emericella	Q9req6 zymomonas m		P40848 schizosacch	Q25479 manduca sex		_		P51002 vibrio para		Q04649 mesocricetu	026918 methanobact	O51038 borrella bu		P16046 simian cyto	P52369 equine herp	P37710 enterococcu		595	315	P55013 squalus aca
SUMMARIES		ΙD	Y33B_MYCPN	QA1S_NEUCR	YJL3_YEAST	CDX2_HUMAN	TSCC_PSEAM	VP50_BPAPS	AROE_SYNY3	Y030_NPVOP	PYRG_AZOBR	SYV_STRCO	CARA_METJA	CDX2_MOUSE	UAPA_EMENI	PURL_ZYMMO	PULA_THEMA	DHP1_SCHPO	NKCL_MANSE	ADB2_YEAST	YMEB_METEX	DCOP_LACLC	OMPK_VIBPA	RIP1_MOMCH	CDX2_MESAU	Y830_METTH	SYW_BORBU	VG10_BPMD2	VP40_SCMVC	VP40_HSVE2	ALYS_ENTFA	EF2_PYRAB	EF2_PYRHO	PRTT_PORGI	NKC1_SQUAC
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RESULT 2
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AC P11637;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)

9 LKQDWNGV 16 |||||||||

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•	39.8 2907 39.8 2911 39.3 39.3 347 39.3 39.3 39.3 39.3 39.8 39.8 39.8 88.8 280 38.8 280 38.8 300 38.8 300		STANDARD;	Rel. 39, Rel. 39, Rel. 40, PROTEIN M	MPN483 OR MP359. Mycoplasma pneumoniae. Bacteria; Firmicutes; Bacill: Mycoplasmataceae; Mycoplasma MyCGBI_TaxID=2104;	[1] SEQUENCE FROM N.A. STAIN-ATCC 29342 / M129; MEDLINE=97105885; Pubmed-8948633; Himmelreich R., Hilbert H., Plage	mann R.; plete sequence analysis of the gamoniae."; eic Acids Res. 24:4420-4449(1996 SIMILARITY: BELONGS TO THE GLYCO. STRONG, TO M.GENITALIUM MG335.2.	This SWISS-PROT entry is copybetween the Swiss Institute the European Bioinformatics I use by non-profit institut modified and this statement inties requires a license entities requires to licensee or send an email to licensee	EMBL; AE000034; AAB96007.1; InterPro; IPR001173; Glycos_transf_Pfam; PF00535; Glycos_transf_2; 1. Hypothetical protein; Transferase; Complete proteome. SEQUENCE 341 AA; 40414 MW; C20	48.0%; Similarity 100.0%; 8; Conservative
	23.33.33.33.33.33.33.33.33.33.33.33.33.3		RESULT 1 Y33B_MYCPN ID Y33B_MYCPN	30-MAY-2000 (30-MAY-2000 (20-AUG-2001 (HYPOTHETICAL	MPN483 OR MP359. Mycoplasma pneumoniae Bacteria; Firmicutes; Mycoplasmataceae; Myc NCBI_TaxID=2104;	[1] SEQUENCE FROM N.A. STRAIN-ATCC 29342 MEDLINE-97105885; Himmelreich R., Hi	Herrmann R.; "Complete seq pneumoniae."; Nucleic Acids -!- SIMILARIT STRONG, T	This SWISS-I between the the European use by nor modified and entities rec	EMBL, ACOUND InterPro; IP Pfam, PF0053 Hypothetical Complete pro	y Match Local hes
			RESULT Y33B_M ID Y	7 7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	S S S S S S	RR RX R	RA RI CC CC	388888888	S K K W B B B B B B B B B B B B B B B B B	Quer Best Matcl

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A; 100580 MW; 67EDA399CBF098B2 CRC64;
                                                                                                             STRAIN=74-0R23-1A;
MEDLINE=89293848; PubMed=2525625;
Geever R.F., Huiet L., Baum J.A., Tyler B.M., Patel V.B.,
Rutledge B.J., Case M.E., Giles N.H.;
"DNA sequence, organization and regulation of the qa gene cluster of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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MEDLINE=97103775; PubMed=8948101;
MEDLINE=97103775; PubMed=8948101;
Sequencing analysis of a 40.2 kb fragment of yeast chromosome X reveals 19 open reading frames including URA2 (5' end), TRK1, PBS2, PST10, GCD14, RPE1, PH086, NCA3, ASF1, CCT7, GZF3, two tRNA genes, three remnant delta elements and a Ty4 transposon.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordarlomycetes;
Sordarlales; Sordarlaceae; Neurospora.
NCBL_TAXID=5141;
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FUNCTION: REPRESSOR FOR ENZYMES AND PROTEINS OF QUINATE
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
TYANSPOSON TY4 20,77 KDA HYPOTHETICAL PROTEIN
01-FEB-1991 (Rel. 17, Last annotation update) QUINATE REPRESSOR.
                                                                                                                                                                                                                                                                                                                                      EMBL, X14603; CAA32753.1; -...
PIR; S0425; S04255.
FIR; E31277; E31277.
InterPro; IPR001381; DHquinase_I.
InterPro; IPR000503; Shik_Kinase.
InterPro; IPR002007; Shik_Kinase.
Féan; PF01487; DHquinase_I:
Féan; PF01488; Shikinate_DH; I.
Féan; PF01202; SKI; I.
Pfan; PF01202; SKI; I.
SEQUENCE 918 AA; 105080 MW; 67ED
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Best Local Similarity
Matches 8; Conserv
                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                            Neurospora crassa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4932;
                                                                                                                                                                                                               METABOLISM.
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TISSUBLE-COLON Carcinoma;
MADILINE-97188282; PubMed=9036867;
Mallo G.V., Rechreche H., Frigerio J.M., Rocha D., Zweibaum A.,
Lacasa M., Jordan B.R., Dusetti N.J., Dagorn J.C., Tovanna J.L.;
Molecular cloning, sequencing and expression of the mRNA encoding
human Cdxl and Cdx2 homeobox. Down-regulation of Cdxl and Cdx2 mRNA
expression during colorectal carcinogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDX2_HUMAN STANDARD; PRT; 311 AA.
099626, 000503.
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1999 (Rel. 38, Last annotation update)
HOWEOBOX PROTEIN CDX-2 (CAUDAL-TYPE HOMEOBOX PROTEIN 2) (CDX-3).
CDX2 OR CDX3.
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SGD; S0003649; YJLJ13W.
InterPro; IPR001584; Rve.
InterPro; IPR001878; Znf_CCHC.
Pfam; PF00665; rve; 1.
SMART; SM00343; Znf_CCHC, 1.
Transposable element; Hypothetical protein.
SEQUENCE 1803 AA; 207693 WW; 16DCD7284A8B552D3 CRC64;
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Pred. No. 57;
1; Mismatches
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EMBL; Y13709; CAA74038.1; -.
HSSP: P02833; ISAN.
MIM; 600297; -.
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Best Local Similarity 69.2%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                              Gaps
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MEDLINE-9319361; PubMed=8464884;
Gamba G., Saltzberg S.N., Lombardi M., Miyanoshita A., Lytton J.,
Hediger M.A., Brenner B.M., Hebert S.C.;
"Primary structure and functional expression of a cDNA encoding the
thiazide-sensitive, electroneutral sodium-chloride cotransporter.";
Proc. Natl. Acad. Sci. US. A. 90:2749-2753(1993).
-I- FUNCTION: ELECTRICALLY SILENT TRANSPORTER SYSTEM WHICH IS A
MEDIATOR OF SODIUM AND CHLORIDE REABSORPTION.
-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-I- SIMILARITY: BELONGS TO THE SLC12A FAMILY OF TRANSPORTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                ol-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
THIAZIDE-SENSITIVE SODIUM-CHLORIDE COTRANSPORTER (NA-CL SYMPORTER).
SIC12A3 OR TSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes; Pleuronectoidei; Pleuronectidae; Pseudopleuronectes. NCBI_TaxID=8265;
                                                                                                                                                                                                                                                                                             2;
                                                                                                         protein; Nuclear protein.
                                                                                                                                                                                                                                                                   Score 42; DB 1; Length 311;
                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                    Q -> AA (IN REF. 2).
A -> AA (IN REF. 2).
A -> G (IN REF. 2).
C2FEDEF1089D2367 CRC64;
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2; Mismatches
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Interpro; IPR002027; Amino_acid_permease.
Interpro; IPR002948; NaCl_trnsportr.
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POLY-PRO.
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                                                                                                                                                HOMEOBOX
                                    PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00021; HTHEPRESSR.
SMART; SM0389; HOX; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS0017; HOMEOBOX_2; 1.
PROSECTE; PS0017; HOMEOBOX_2; 1.
PROMEORY; DANA-binding; Developmental DOMAIN
InterPro; IPR000047; HTH_repressr.
InterPro; IPR001356; Homeobox.
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(Rel. 34, Last seq
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PRINTS; PR01230; NACLTRNSPORT.
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            InterPro; IPR001356; Homeobo
Pfam; PF00046; homeobox; 1.
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93
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01-0CT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              van der Wilk F., Dullemans A.M., Verbeek M., van den Heuvel J.F.J.M.;
"Isolation and characterization of APSE-1, a bacteriophage infecting
the secondary endosymbiont of acyrthosiphon pisum.";
ViroLogy 262:104-113(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       INKED (GLCNAC. . .) (POTENTIAL).
69AE2D53B8F84D89 CRC64;
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N-LINKED (GLCNAC.
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
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Pred. No. 39;
1; Mismatches
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58.3%;
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727 PNVLLMGFKKDW 738
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Best Local Similarity
T; Conserve
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767
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Q9T1P8;
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us-09-765-739a-4.rsp

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                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-97271300; PubMed=9126251;
Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
Rohrmann G.F.;
The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear
Phyledrosis virus genome.";
Virology 229:381-399(1997).

- SIMILARITY: TO CORRESPONDING ORF IN ACMNPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STEADURACE FROM N.A.
STRAIN-ATCC 29145 / SP7;
MEDLINE-94186025; PubMed=8138139;
MEDLINE-94186025; PubMed=8138139;
MEDLINE-94186055; PubMed=8.7
Indentification and sequencing of pyrG, the CTP synthetase gene of Azospitilum brasilense Sp7.";
FEMS Microbiol. Lett. 115:723-738(1994).
I- CATALYTIC ACTIVITY: ATP + UTP + GUTAMINE = ADP + ORTHOPHOSPHATE.
CTP (AMMONIA CAN REPLACE GLUTAMINE).
I- EMEXIME REGULATION: ACTIVATED BY GTP AND INHIBITED BY CTP.
I- PATHWAY: LAST STEP IN PYRIMIDINE BLOSYNTHESIS.
I- SIMILARITY: TO OTHER SPECIES CTP SYNTHASE.
I- SIMILARITY: THE GATASE DOMAIN BELONGS TO TYPE-1 GLUTAMINE
AMIDOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE).
           O10293;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 52.7 KDA PROTEIN (ORF38).
OFRYJA pseudotsugata multicapsid polyhedrosis virus (OPMNPV).
Viruses; dsDNA viruses, no RNA stage; BaculoViridae;
Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Azospirillum brasilense.
Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;
Azospirillum:
NCBI_TaxID=192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 1; Length 459;
Pred. No. 25;
Mismatches 4; Indels
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459 AA; 52731 MW; DAAFBD8C6628F596 CRC64;
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Best Local Similarity 53.3
Matches 8; Conservative
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MEDILINE—97061201; PubMed-8905231;

Rancko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,

Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,

Hisosuchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.

Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence analysis of the genome of the unicellular cyanobacterium
Synchocystis Sp. strain PCG803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions.";
DNA Res. 3:109-136(1996).
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0
                                                                                                     Score 41; DB 1; Length 184;
Pred. No. 9.6;
1; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                               20416 MW; EB705FA272B6768F CRC64;
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InterPro: IPRO02907; Shikimate DH.
Pfam; PFO448; Shikimate DH. 1
Aromatic amino acid biosynthesis; Oxidoreductase; NADP;
COMPLETE Protecome.
SEQUENCE 290 AA; 31099 MW; 8A2D38EE5D57B303 CRC64;
                                                                                                                                                                                                                                                                                                          20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SHIKINATE 5-DEPUPROGENASE (EC 1.1.1.25).
Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chrococcaies; Synechocystis.
NCBL_TAXID-1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31099 MW; 8A2D38EE5D57B303 CRC64;
                                                                                                                                                                                                                                                                                    290 AA
             EMBL; AF157835; AAF03993.1;
Hypothetical protein.
SEQUENCE 184 AA; 20416 MM
                                                                                                   / Match 41.8%;
Local Similarity 50.0%;
les 9; Conservative
                                                                                                                                                                                            128 NATVEFYGYDNNGKGVSA 145
                                                                                                                                                             1 NPTVALYGLKQDWNGVSA 18
                                                                                                                                                                                                                                                                                STANDARD;
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                            AROE_SYNY3
P74591;
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ID Y030_NPVOP
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Matches
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S KW SO
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459 AA

STANDARD;

6 A

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Gaps

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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=A3(2) / M445;
MEDLINE=98164371; PubMed=9503623;
Burger A., Brandt B., Suesstrunk U., Thompson C.J., Wohlleben W.;
Analysis of a Streptomyces coelicolor A3(2) locus containing the nucleoside diphosphate kinase (ndk) and folylpolyglutamate synthetase (folc) genes.";
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                        SIV_STRCO STANDARD, PRT; 874 AA.

008851, 901LG3;
15-JUL-1998 (Rel. 36, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
VALXI-TRNA SYMTHETASE (EC 6.1.1.9) (VALINE--TRNA LIGASE) (VALRS).
VALS OR SCC88.26G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces NCBL_TaxID=1902;
                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saunders D., Harris D., Cerdeno A.M., Parkhill J., Barrell B.G. Rajandream M.A.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                         EMBL, X67216, CAA47656.1, -.
PIR: S25101; S25101.
InterPro: IPPR000991; GATase_1.
Pfam: PF00117; GATase; 1.
PROSITE; PS00442; GATASE_TYPE_I; 1.
Pymindine blosynthesis; Ligase; Glutamine amidotransferase.
                                                                                                                                                                                                                 Score 41; DB 1; Length 544; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FERS MICROBIOL. Lett. 159:283-291(1998).

-!- CATALYTIC ACTIVITY: ATP + L-VALINE + TRNA(VAL) = AMP PYROPHOSPHATE + L-VALYL-TRNA(VAL).

-!- SUBGNIT: MONOMER (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                            5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                NTASE (BY SIMILARITY).
13AA1A8B8EB6C5DB CRC64;
                                                                                                                                       GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
                                                                                                                                                                                                                                           1; Mismatches
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InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR002303; tRNA-synt_val.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL139298; CAB75396.1; -.
                                                                                                                                                                            544 AA; 59908 MW;
                                                                                                                                                                                                                41.8%;
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                                                                                                                                                                                                                                            7; Conservative
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                                                                                                                                                  516
518
                                                                                                                                                                                                                                                                                            410 NPVVGLLGLMTEW 422
                                                                                                                                                                                                                                                                   1 NPTVALYGLKQDW 13
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Best Local Similarity
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SEQUENCE FROM N.A.
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518
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ACT_SITE
SEQUENCE
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MEDLINE-9637999; PubMed-868087;
MEDLINE-9637999; PubMed-868087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.E., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
Pfam; PF00133; LRNASYNTHVAL.
PRINTS; PR00986; TRNASYNTHVAL.
PROSITE; PS00178; AA_TRNA_LIGASE_I; PARTIAL.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Last sequence update)
CAGG-2001 (Rel. 40, Last annotation update)
CARBAMOYL-PHOSPHATE SYNTHASE SMALL CHAIN (EC 6.3.5.5) (CARBAMOYL-PHOSPHÄTE SYNTHESTE GLUTAMINE CHAIN).
                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                          Score 41; DB 1; Length 874;
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                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                         "KWSKS" REGION.
ATP (BY SIMILARITY).
KL -> NV (IN REF. 1).
AD11E4871786BAAO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          354 AA
                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                   Pred. No.
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Interpro; IPR002474; CPSase_sm_cha
Interpro; IPR000991; GATase_1.
Pfam; PF000988; CPSase_sm_chain; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 35, Created)
                                                                                                                                                                                                             97566 MW;
                                                                                                                                                                                                                                                                                             41.8%;
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                                                                                                                                                                                                                                                                                                                   53.8%;
                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 53.87
ابت 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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517 TIALHGMVRDQNG 529
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                                                                                                                                                                                 638 6
874 AA;
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-! PUOTION: MAY BE NECESSARY FOR SOME GENERAL ASPECT OF COLONIC EPITHELIAL PHENOTYDE.

-! SUBCELLULAR LOCATION: NUCLEAR.
-! TISSUE SPECIFICALLY: INTESTINE; EXPRESSED SPECIFICALLY IN GUT EPITHELIUM WHERE IT IS NOT RESTRICTED TO A PARTICULAR CELL LINEAGE. ABUNDANT EXPRESSION IS SEEN IN THE PROXIMAL COLON WITH SLIGHTLY LOWER LEVELS IN DISTAL COLON. EXPRESSION IN THE PROXIMAL COLON IS NOT RESTRICTED EITHER TO A PARTICULAR CELL LINEAGE OR STAGE OF DIFFERENTIATION WHILE IN THE DISTAL COLON IT SIN MORE STAGE OF DIFFERENTIATION WHILE IN THE DISTAL COLON IT IS MORE ABUNDANT IN THE DIFFERENTIATED CELLS TOWARDS THE TOP OF THE CRYPT.
-! SIMILARITY: BELONGS TO THE CAUDAL FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECHENCE FROM N.A.
SECHENCE FROM N.A.
MEDLINE-94253086; PubMed-7910823;
James R.J., Erler T., Kazenwadel J.;
Structure of the muxine homeobox gene cdx-2. Expression in embryonic and adult intestinal epithelium.";
J. Biol. Chem. 269:15229-15237(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-Small intestine;
MEDLINE-95021263; Pubmed-7935448;
Sub E., Chen L., Taylor J., Traber P.G.;
"A homeodomain protein related to caudal regulates intestine-specific
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           James R.J., Kazenwadel J.; "Homeobox gene expression in the intestinal epithelium of adult
                                                                                                                                                                                                                          3;
                                                                                                                                                                                           DB 1; Length 354;
                                                                                                                                                                                                                        5; Indels
                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HOWEOBOX PROTEIN CDX-2 (CAUDAL-TYPE HOMEOBOX PROTEIN 2).
                                                                                                         GLUTAMINE AMIDOTRANSFERASE.
GATASE (BY SIMILARITY).
4D8F07776CA65F9F CRC64;
Pfam; PF00117, GATase; 1.
PRINTS; PR00096; GATASE; PRINTS; PR00099; CPSGATASE.
PROSITE; PS00442; GATASE_TYPE_I; FALSE_NEG.
Arighnine biosynthesis; Pyrimidine biosynthesis; Ligase; Complete protecome.
                                                                                                                                                                                                                                                                                                                                                                   PRT; 311 AA.
                                                                                                                                                                                           41.3%; Score 40.5; I
40.0%; Pred. No. 23;
ative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene transcription.";
Mol. Cell. Biol. 14:7340-7351(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 204-229 FROM N.A. MEDLINE=91131633; PubMed=1671571;
                                                                                                           7 354 G
250 250 G
354 AA; 39920 MW;
                                                                                                                                                                                                                                                      2 PTVALYGLKQDW---NGVSA 18
                                                                                                                                                                                                                                                                                     56 PLEGNYGVKKDWFESDGIKA 75
                                                                                                                                                                                         Query Match
Best Local Similarity 40.0
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDX2 OR CDX-2.
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                                                                                                                           ACT_SITE
SEQUENCE
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CDX2_MOUSE
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Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-1- INDUCTION: INDUCIBLE BY 2-THIOURIC ACID, AND HIGHLY REPRESSIBLE BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                             AMMONIUM.
-!- SIMILARITY: BELONGS TO THE XANTHINE/URACIL PERMEASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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MEDILINE-94043131; PubMed-8226862;
Gorfinkiel L., Diallinas G., Scazzocchio C.;
"Sequence and regulation of the uapA gene encoding a uric acid-
xanthine permease in the fungus Aspergillus nidulans.";
J. Biol. Chem. 268:23376-23381(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungl; Ascomycota; Pezizomycotina; Eurotiomycetes;
Burotiales; Trichocomaceae; Emericella.
NCBL_TaxID=5072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40; DB 1; Length 311;
Pred. No. 24;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> H (IN REF. 2).
71FFC4C263462FF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1994 (Rel. 30, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
UNIC ACID-XANTHINE PERMEASE (UAPA TRANSPORTER).
UAPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-GLN.
Y -> H (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOMEOBOX
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247 257 P
69 69 Y
311 AA; 33476 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 40.8%;
Best Local Similarity 56.2%;
Matches 9; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X71807; CAA50681.1; -.
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Q07307;
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DOMAIN
CONFLICT
SEQUENCE
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UPA_EMBNI
1D 01-0217
DT 01-0217
DT 15-JUL
DE UNIC 07-0217
DE UNIC 05
DE UNIC 0
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Query Match
Best Local Similarity
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                                                                                                                     PULA_THEMA
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ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACT_SITE
                                                                                                                               033840;
                                                                                               RESULT 15
PULA_THEMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGR;
                      Matches
                                            õ
                                                               qq
                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UM H.W., Kang H.S.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + 5'-PHOSPHORIBOSYLFORNYLGIYCINAMIDE +
L-GLUTAMINE + H(2)O = ADP + ORTHOPHOSPHATE + 5'-PHOSPHORIBOSYL-
                                                                                                                                                                                                                                                                                                                                                                            20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM
                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (POTENTIAL).
E56A984D956897E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Zymomonas mobilis.
Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
                                                                                                                                                                                                                                                  . 9
                                                                                                                                                                                                                            Score 40; DB 1; Length 615;
Pred. No. 49;
                                                                                                                                                                                                                                                  5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FORMYLGLYCINAMIDINE + L-GLUTAMATE.
-!- PATHWAX: DE NOVO PURINE BIOSYNTHESIS: FOURTH STEP.
-!- SUBUNIT: HETERODIMER OF TWO SUBUNITS, PURQ AND PURL.
-!- SUBCELLUAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE FGAMS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 117 ATP (POTENTIAL).
734 AA; 77679 MW; B771635E0F66A166 CRC64;
                                                                                                                                                                                                                                                                                                                                               734 AA.
                                ä
                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Purine biosynthesis; Ligase; ATP-binding.
        Interpro; IPR000444; Xan_ur_permease.
Pfam; PF00860; Xan_ur_permease; 1.
PROSITE; PS01116; XANTH_URACIL_PERMASE;
                                                                        POTENTIAL. POTENTIAL.
                                                                                                                   POTENTIAL. POTENTIAL.
                                                                                             POTENTIAL. POTENTIAL.
                                                   POTENTIAL.
                                                               POTENTIAL.
                                                                                                                                        POTENTIAL.
                                          Glycoprotein
                                                                                                                                                               POTENTIAL
                                                                                                                                                                        POTENTIAL
                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF213822; AAF23789.1; -.
InterPro; IPR000728; AIRS_related.
Pfam; PF00586; AIRS; 2.
                                                                                                                                                                                                                                                                                   266 PTVMLIGISLIGTGFKDWAGGSA 288
                                                                                                                                                                                                                                                                      2 PTVALYGLK-----QDWNGVSA 18
                                                                                                                                                                                                                                                                                                                                                                20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last seq
20-AUG-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=ATCC 31821 / ZM4 / CP4;
                                                                                                                                                                                             MM:
                                                                                                                                                                                                                            40.8%;
                                          Transport; Transmembrane;
                                                                                                                                                                                             65453
                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                               STANDARD;
S36031; S36031
                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                  10
615 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=542;
                                                                                                                                                                                                                                                                                                                                                                                                             SYNTHASE II).
                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                               PURL_ZYMMO
Q9REQ6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zymomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NP_BIND
SEQUENCE
                                                   TRANSMEM
TRANSMEM
                                                                                     TRANSMEM
                                                                                                        TRANSMEM
                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                             Query Match
                                                                        TRANSMEM
                                                                                               TRANSMEM
                                                                                                                    TRANSMEM
                                                                                                                             TRANSMEM
                                                                                                                                          TRANSMEM
                                                                                                                                                   TRANSMEM
                                                                                                                                                                        FRANSMEM
                                                                                                                                                                                                                                                                                                                          RESULT 14
PURL_ZYMMO
                                                                                                                                                                                                                                                                                                                                                                                                                         PUR-Q
                                                                                                                                                                                                                                                Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.ch).
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                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAY-2000 (Rel. 39, Last sequence update)
20-MAG-2001 (Rel. 40, Last annotation update)
BULLULANASE PRECURSOR (EC 3.2.1.41) (ALPHA-DEXTRIN ENDO-1,6-ALPHA-GLUCOSIDASE) (PULLULAN 6-GLUCANOHYDROLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bibel M., Brettl C., Gosslar U., Kriegshaeuser G., Liebl W.; "Isolation and analysis of genes for amylolytic enzymes of the hyperthermophilic bacterium Thermotoga maritima."; FEMS Microbiol. Lett. 158:9-15(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: STARCH-DEBRANCHING ENZYME, HYDROLYSES (1-6)-ALPHA-GLUCOSIDIC LINKAGES IN PULLULAN AND STARCH TO FORM MALTOTRIOSE.
DB 1; Length 734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 843;
                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C42DDE233D54FE77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase; Glycosidase; Signal; Complete proteome. SIGNAL 1 19 POTENTIAL.
                                                                                         4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           843 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40;
Pred. No. 6
    Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Thermotogales; Thermotoga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000461; Alpha_amylase.
Pfam; PF00128; alpha-amylase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=MSB8 / DSM 3109;
MEDLINE=98115241; Pubmed=9453151;
                                                                                         ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ001087; CAA04522.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96261 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.8%;
    40.8%;
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                                                                                    7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         843
535
564
652
                                                                                                                                                                                                                                                         550 PTIGGVGLLQDW 561
                                                                                                                                                                    2 PTVALYGLKQDW 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermotoga maritima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    564
652
843 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=2336;
```

2; Gaps 1;

5; Indels

us-09-765-739a-4.rsp

Search completed: March 14, 2002, 09:24:51 Job time: 907 sec

Matches 8; Conservative 3; Mismatches

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

Search time 56.96 Seconds March 14, 2002, 09:10:42; Run on:

(without alignments)
26.747 Million cell updates/sec

US-09-765-739A-3 107

1 NTTVGVFGLKQNWDGSAISN 20 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir1:* pir2:* pir3:* pir4:* PIR_68:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Query	Query Match Length	DB	ID	, Description
1	107	100.0	276	. 7	JE0218	28k surface antige
7	91	85.0	280	N	JE0217	surface anti
3	73	68.2	286	7	JE0219	surface
4	61.5	57.5	133	7	JE0221	28k surface antige
2		56.1	278	7	JE0216	surface
9	53	49.5	284	7	I40882 .	major antigenic pr
7		43.0	299		T23932	hypothetical prote
8		43.0	1004		JH0470	Na+/K+-exchanging
6	46	43.0	1034		S76134	hypothetical prote
10	45	42.1	160		A75466	2-demethylmenaguin
11	45	42.1	300		S60558	envelope polyprote
12	45	42.1	300		S60526	envelope polyprote
13	45	42.1	490		G85354	hypothetical prote
14	45	42.1	540		S54586	probable membrane
15	44	41.1			A56594	Na+/K+-exchanging
16	4	41.1			C86822	hypothetical prote
17	43.5	40.7		7	G83166	
18	43	40.2	86	7	S28126	gas-vesicle protei
19	43	40.2		~	T40502	hypothetical prote
20	43	40.2		7	S73667	adhesin P1 precurs
21	43	40.2	4	7	873379	adhesin Pl precurs
22	43	40.2		7	S73952	adhesin Pl precurs
	43	40.2	L.	7	E81017	ABC transporter, A
	4	40.2		П	P3BPF6	P3 protein - phage
25	42.5	39.7		7	C82096	aminoacyl-histidin
		39.7	-	7	873296	glutamate synthase
27	42	39.3		7	545	probable membrane
28	42	39.3	297	~	T21632	hypothetical prote
29	42	39.3	467	7	S30839	

hypothetical prote	Na+/K+-exchanging	probable PRP19-lik	streptothricine ac	ribosomal protein	hypothetical prote	biotin synthetase	biotin synthetase	hypothetical prote	hypothetical prote	hypothetical prote	(2'-5')oligo(A) sy	(2'-5')oligo(A) sy	acetyltransferase	(2'-5')oligo(A) sy	(2'-5')oligo(A) sy
T20037	S03632	C84744	862939	T06915	T13743	F64695	н71823	S76408	C72239	T25499	SYMS02	SYHU16	F69008	SYHU18	SYMS03
631 2	38 I	340 2	73 2	33 2	64 2	82 2	82 2	30 2	131 2	157 2	163 1	164 1	177 2	00 1	14 1
39.3	_														
42	42	41.5	41	41	41	41	41	41	41	41	41	41	41	41	41
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Descriptions and the second state of the second sec

ö Gaps ö Length 276; Indels Score 107; DB 2; Pred. No. 1.2e-09; Mismatches 0; Query Match 100.0%; S
Best Local Similarity 100.0%; P
Matches 20; Conservative 0;

1 NTTVGVFGLKQNWDGSAISN 20 59 NTTVGVFGLKQNWDGSAISN 78 ò

g

Gaps ó Length 280; Query Match 85.0%; Score 91; DB 2; Length 280 Best Local Similarity 84.2%; Pred. No. 4.6e-07; Matches 16; Conservative 2; Mismatches 1; Indels

ó;

1 NTTVGVFGLKQNWDGSAIS 19 ò

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Na+/K+exchanging ATPase (EC 3.6.1.37) alpha chain (clone pArATNa136) - brine shrimp C; Species: Artemia franciscana (brine shrimp)
C; Date: 30-Jun-1992 **sequence_revision 30-Jun-1992 **text_change 22-Jun-1999 C; Accession: JH0470; S24196
R; Macias, M.T.; Palmero, I.; Sastre, L. Gene 105, 197-204, 1991
A; Tille: Cloning of a CDNA encoding an Artemia franciscana Na/K ATPase alpha-subunit. A; Reference number: JH0470; MUID:92039032
                                                                                                                                                 major antigenic protein - heartwater rickettsia
Cispecies: Cowdria ruminantium (heartwater rickettsia)
Cispecies: Cowdria ruminantium (heartwater rickettsia)
Ciscossion: 140882; S42827
Ciscossion: 140882; S42827
Ciscossion: 140882; A.H.; Jongejan, F.; van Kleef, M.; van der Zeijst, B.A.
Infect. Immun. 62, 1451-1456, 1994
A; Title: Modecular cloning, sequence analysis, and expression of the gene encoding the Reference number: 140882; MUID:94178956
A; Reference number: 140882; MUID:94178956
A; Reference treatment; translated from GB/EMBL/DDBJ
A; Molecula type: DNA
A; Molecula type: DNA
A; Cross-references: EMBL:X74250; NID:9454266; PIDN:CAA52309.1; PID:9454267
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein ROSD7.4 - Caenorhabditis elegans
C;Specias: Genochabditis elegans
C;Specias: Genochabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T23932 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T23932 #sequence_revision 15-Oct-1996
A;Recession: T23932
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T23932
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-299 *WIL>
A;Residues: 1-299 *WIL>
A;Cossion: T299 *WIL>
A;Cossion: T299 *WIL>
A;Cossion: T290 *WIL>
A;Cossion: T290 *WIL>
A;Cossion: T290 *WIL>
A;Cossion: T290 *WIL>
A;Coserimental source: Clone ROSD7.4
A;Coserimental source: Clone ROSD7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 53; DB 2; Length 284;
Pred. No. 0.58;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 46; DB
Pred. No. 8.1;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162/1; 231/2; 268/3
49.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 43.0%;
Best Local Similarity 56.2%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 1
A;Introns: 29/3; 122/1; 162/1.
C;Superfamily: tropinesterase
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53 GLFGQKQNWNSVGKAL 68
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N.Alternate names: MAPI
C; Species: Ehrlichia chaffensis
N.Alternate names: MAPI
C; Species: Ehrlichia chaffensis
C; Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 17-Mar-1999
C; Accession: JE0216
C; Accession: JE0216
Biochem. Biophys. Res. Commun. 247, 636-643, 1998
A; Title: Molecular characterization of a 28kpa surface antigen gene family of the tribe A; Accession: JE0216
A; Molecule type: DNA
A; Residues: 1-278 < RED>
A; Residues: 1-278 < RED>
A; Cross-references: GB: AF062761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28k surface antigen 2 - Ehrlichia chaffensis
NiAlternate names: MAPI
NiAlternate names: MAPI
C;Species: Ehrlichia chaffensis
C;Decies: Ehrlichia chaffensis
C;Date: 21-Mar-1999
C;Accession: JE0219
R;Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Biochem. Biophys. Res. Commun. 247, 636-643, 1998
A;Title: Molecular characterization of a 28kDa surface antigen gene family of the tribe A;Reference number: JE0216; MUID:98321180
A;Recession: JE0219
A;Residues: 1-286 < RED>
A;Residues: 1-286 < RED>
A;Cross-references: GB:AF062761
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                                                                                                                                                                                                                                                                                                                                                                                                                                      68.2%; Score 73; DB 2; Length 286 ilarity 68.4%; Pred. No. 0.00037; Conservative 3; Mismatches 3; Indels
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62 TTV-VYGLKENWAGDAISS 79
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Matches 13; Conserv
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Cincesions, W.; Heydrickx, L.; Van de Peer, Y.; Bouckaert, A.; Fransen, K.; Motte, J. Alossens, W.; Heydrickx, L.; Van de Peer, Y.; Bouckaert, A.; Fransen, K.; Motte, J. Alos 8, 21-26, 1994
A.;Title: Molecular phylogeny of part of the env gene of HIV-1 strains isolated in Cot A; Reference number: S60521; MUID:94280700
A; Status: nucled: caid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-300 <JAN>
A; Residues: 1-300 <JANA
A; Residues: 
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                                                                                                                                                                                                                                                                                                                                                                                  GB:AE000513; NID:g6458577; PIDN:AAF10437.1; PID:g645
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A.Title: Genome sequence of the radiocesistant bacterium Deinococcus radiodurans Rl.
A.Reference number: A75250; MUID:20036896
A.Reference number: A75466
A.Status: prealiminary
A.Rolecule type: DNA
A.Residues: 1-160 <WHI>
A.C. Sareferences: GB:AE001940; GB:AE000513; NID:g6458577; PIDN:AAF10437.1; PID:g64;
A.C. Sareferences: GB:AE001940; GB:AE000513; NID:g6458577; PIDN:AAF10437.1; PID:g64;
A.C. Sareferences: A.C. Sareferences: Strain Rl
C. Genetics: A.C. Sareferences: Strain Rl
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A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-300 <a href="https://dxf">A;Residues: 1-300 <a href="https://dxf">A;Residues: 1-300 <a href="https://dx">A;Residues: 1-300 <a href="https://dx">https://dx</a>
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C,Superfamily: type E retrovirus env polyprotein
C,Keywords: AIDS; glycoprotein; immunodeficiency;
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4; Mismatches
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117 TSGLFNSTWNWNGTAIT 133
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C; Keywords: methyltransferase
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                                               C;Accession: A75466
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
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A; Cross-references: EMBL:D90914; GB:AB001339; NID:g1653477; PIDN:BAA18393.1;
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June C; Superfamily: phosphoenolpyruvate carboxylase
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A; Variety: PCC 6803
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
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C;Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Sep-2000
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$\frac{5.57/Active site: Asp (aspartylphosphate intermediate) #status predicted
$F;489/Binding site: ATP (Lys) #status predicted
$F;698,702,707/Active site: Asp, Asp, Lys #status predicted
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Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           intracellular #status predicted <INT4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;937-955/Domain: transmembrane #status predicted <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 46; DB 2;
Pred. No. 30;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.0%;
40.0%;
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50.0%;
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864 LFGLRKHWDSRAVND 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NLAVPAFGLSTNWSGN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 VFGLKQNWDGSAISN 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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Best Local Similarity
Matches 8; Conserv
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                  A; Accession: JH0470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S76134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;856-936/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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A; Residues: 1-540 <PEA>
A; Cross-references: EMBL:249704: NID:g825540; PIDN:CAA89777.1; PID:g825545; GSPDB:GNO
A; Experimental source: strain AB972
C; Genetics:
A; Gene: MIPS:YMR279c
A; Map position: 13R
C; Superfamily: aminotriazole resistance protein YML116w
C; Superfamily: aminotriazole resistance protein Prilon: 13R
C; Superfamily: aminotriazole resistance protein Prilon: 13P
C; Superfamily: aminotriazole resistance protein Prilon: 13P
C; Superfamily: aminotriazole resistance predicted <TM2>
F; 109-125, Domain: transmembrane #status predicted <TM3>
F; 109-125, Domain: transmembrane #status predicted <TM3>
F; 238-244, Domain: transmembrane #status predicted <TM6>
F; 238-344, Domain: transmembrane #status predicted <TM6>
F; 238-34, Domain: transmembrane #status predicted <TM8>
F; 377-393, Domain: transmembrane #status predicted <TM8>
F; 377-393, Domain: transmembrane #status predicted <TM8>
F; 377-394, Domain: transmembrane #status predicted <TM8>
F; 377-395, Domain: transmembrane #status predicted <TM8>
F; 377-395, Domain: transmembrane #status predicted <TM10>
F; 503-519, Domain: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 540;
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: March 14, 2002, 09:10:43 Job time: 359 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NTTVGVFGLKQNWDGSAIS 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 42.1
Best Local Similarity 36.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LFGIRKQWDSKAVND 911
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                                                          envelope polyprotein gp41 - human immunodeficiency virus type 1 (isolate CI-330-3) (frage cyclope polyprotein gp41 - human immunodeficiency virus type 1 (isolate CI-330-3) (frage CSpecies; human immunodeficiency virus type 1, HIV-1

A; Variety: isolate CI-330-3

C; Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999

C; Accession: 860226

R; Janssens, W.; Heyndrickx, L.; Van de Peer, Y.; Bouckaert, A.; Fransen, K.; Motte, J.;

A; Danssens, W.; Heyndrickx, L.; Van de Peer, Y.; Bouckaert, A.; Fransen, K.; Motte, J.;

A; Danssens, W.; Heyndrickx, L.; Van de Peer, Y.; Bouckaert, A.; Fransen, K.; Motte, J.;

A; Danssens, W.; Heyndrickx, L.; Van de Peer, Y.; Bouckaert, A.; Fransen, K.; Motte, J.;

A; Reference number: S60221; MUID:94280700

A; Reference number: S60221; MUID:94280700

A; Residues: 1-300 -374

A; Status: nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA

A; Residues: 1-300 -374

A; Ross-references: EMBL:X72064; NID:9468784; PIDN:CAA50945.1; PID:9468785

A; Roserimental source: isolate CI-330-3

A; Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993

C; Genetics:
A; Genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein AT4930340 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C;Accession: 68354
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin Nature 402, 769-777, 1999
A;Title: Sequence and analysis of Chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488
A;Accession: 685554
A;Accession: 68554
A;Accession: 68554
A;Accession: 67554
A;Canetion: 4040 < 63TO>
A;Cross-references: GB:NC_001268; NID:97269934; PIDN:CAB81027.1; GSPDB:GN00140
A;Map position: 4
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NyAlternate names: hypothetical protein YM8021.05c
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Accession: S54586
S;Pearson, D: Bowman, S.
Submitted to the EMBL Data Library, May 1995
A;Reference number: S54582
A;Accession: S54586
A;Molecule type: DNA
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42.1%; Score 45; DB 2; Length 490;
Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 300;
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Pred. No. 12;
4; Mismatches
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Query Match 42.1%; Best Local Similarity 47.1%; Matches 8; Conservative

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13

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

March 14, 2002, 09:10:43; Search time 56.96 Seconds Run on:

(without alignments)
24.072 Million cell updates/sec

US-09-765-739A-4 98 1 NPTVALYGLKQDWNGVSA 18 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

219241 segs, 76174552 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database :

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	On the contract of the contrac	Surface		antiqe	28k surface antige	phosphoglycerate t	hypothetical prote	28k surface antige	hypothetical prote				regulatory protein	probable nadh oxid	TyB protein - yeas	hypothetical prote	hypothetical prote	immediate-early pr	endo-1,4-beta-xyla	endo-1,4-beta-xyla	hypothetical prote	ß	hypothetical prote	hypothetical prote	probable glutaredo	hypothetical prote			
SUMMARIES	ID	TE0216	TE0217	JE0218	140882	JE0219	E82426	S73685	JE0221	C86822	G64558	T23932	T15839	S04255	G71838	S31262	PC1253	S52611	S56894	\$75205	T43979	T09313	S59631	\$59633	B75622		C64474	195	A72669	m
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	* Query Match Length	278	280	276	284	286	439	341	133	1649	122	299	480	918	328	1465	1467	1802	1803	298	389	412	959	661	691	1023	2894	122	243	290
	& Query Match	10		58.2	9	÷	6	8	46.9	44.9	4	4	43.9	43.9	43.4	43.4	43.4	,	43.4	'n	42.9	ć.	42.9	42.9	7	42.9	42.9	42.3	41.8	41.8
	Score	88	9	57	55	50	48	47	46	44	43.5	43.5	43	43	42.5	42.5	42.5	42.5	42.5	42	42	42	42	42	42	42	42	41.5	41	41
	Result No.		2 1	ım	4	ഗ	9	7	æ	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical prote	hypothetical prote	hypothetical prote	CTP synthase (EC 6	probable acidCoA	hypothetical prote	hypothetical prote	subtilisin-type pr	hypothetical prote	retrovirus-related	carbamoy1-phosphat	pol polyprotein -	probable retroelem	hypothetical prote	hypothetical prote	probable 2-demethy
675073	T18760	T10307	S25101	B75265	A83237	A75595	C84120	T21018	E53226	B64427	S00954	F84486	F83935	нв3068	F82084
2	~	~	N	~	7	7	7	7	7	~	~	7	7	7	7
373	412	459	544	585	624	716	757	1232	83	358	982	1356	105	125	162
41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.3	41.3	41.3	41.3	40.8	40.8	40.8
41	41	41	41	41	41	41	41	41	40.5	40.5	40.5	40.5	40	40	40
30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

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DE0216

28k surface antigen 3 - Ehrlichia chaffensis

28k surface signification and surface antigen gene family of the tri

28k surface signification of a 28k surface antigen gene family of the tri

28k surface sumber: JE0216; MUID:98321180

A. Accession: JE0216

A. Residues: 1-278 < RED>

A. Residues: 1-278 < RED>

A. Cross-references: GB:AF062761
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                                                                                                                                                                                                                                                                                                                                                                                                       89.8%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 89.8
Best Local Similarity 83.3
Matches 15; Conservative
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1 NPTVALYGLKQDWNGVSA 18 60 NPTVALYGLKQDWEGISS 77 ò QQ

JE0217 JE0217 28k surface antigen 4 - Ehrlichia chaffensis N.Alternames: MAPI C:Species: Ehrlichia chaffensis C:Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 17-Mar-1999 C:Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 17-Mar-1999 C:Accession: JE0217 R:Reddy, G.R.: Sulsona, C.R.: Barbet, A.F.: Mahan, S.M.; Burridge, M.J.; Alleman, A.R Biochem. Biophys. Res. Commun. 247, 636-643, 1998 A;Title: Molecular characterization of a 28kDa surface antigen gene family of the tri A;Accession: JE0217 A;Accession: JE0217 A;Molecule type: DNA A;Residues: 1-280 cRED> A;Cross-references: GB:AF062761

Gaps ö 62.2%; Score 61; DB 2; Length 280; 60.0%; Pred. No. 0.023; ive 4; Mismatches 2; Indels Query Match 62.2 Best Local Similarity 60.0 Matches 9; Conservative

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1 NPTVALYGLKQDWNG 15 | |: ::||||||:| 60 NTTIGVFGLKQDWDG 74 δλ q $^{\circ}$

Page

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Gaps

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phosphoglycerate transport system transcription regulator protein PgtA VCA0704 [impor C; Specias: Vibrio choldrae (c) Pacalsa: Vibrio choldrae (c) Date: 18 Aug-2000 #sequence_revision 20 Aug-2000 #text_change 02-Feb-2001 (C) Accession: BSB426 (E) Accession: BSB4426 (E) 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein yibb - Mycoplasma pneumoniae (strain ATCC 29342)
Nylothetical protein protein P01_orf341
C)Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
A;Variety: ATCC 29342
A;Variety: ATCC 29342
C;Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 07-bec-1999
C;Accession: S7388
B;Himmalreich, R;Hilbert, H;Plagens, H;Pirkl, E; Li, B.C.;Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumon A;Recession: S73865
A;Recession: S73865
A;Recession: S73865
A;Recession: A;Re
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A; Molecule type: DNA
A; Mesidues: 1-439 < CHEL>
A; Cross-references: GB: AE04400; GB: AE003853; NID: 99658121; PIDN: AAF96603.1; GSPDB:GN
A; Experimental source: serogroup 01; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A)Cross-references: EMBL:AE000034; GB:U00089; NID:g1674031; PIDN:AAB96007.1; PID:g167
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
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ilarity 100.0%; Pred. No. 5.4;
Conservative 0; Mismatches 0; Indels
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Pred. No. 4.8;
4; Mismatches 4; Indels
      Indels
2;
      Mismatches
2;
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ilarity 50.0%;
Conservative
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      Conservative
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                                                                                                  1 NPTVALYGLKQDWN 14
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60 NTTVGVFGIEQDWD 73
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Best Local Similarity
Matches 8; Conserv
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Matches 8; Conserv
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7;
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A;Gene: VCA0704
A;Map position:
      Matches
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                                                                          28k surface antigen 5 - Ehrlichia chaffensis
28k surface antigen 5 - Ehrlichia chaffensis
N.Alternate names: MAPI
C:Space: Shrlichia chaffensis
C:Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 17-Mar-1999
C:Accession: JEO218
R:Reddy, G. R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Biochem. Biophys. Res. Commun. 247, 636-643, 1998
R:Reddy, G. R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Biochem. Biophys. Res. Commun. 247, 636-643, 1998
R:Reference number: JEO216; MUID:98321180
A:Reference number: JEO216
A:Reference number: DNA
A:Residues: 1-276 cRED>
A:Residues: 1-276 cRED>
A:Cross-references: GB:AF062761
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28k sufface antigen 2 - Ehrlichia chaffensis
28k sufface antigen 2 - Ehrlichia chaffensis
3.A.A.Esbacies: Ehrlichia chaffensis
5.Species: Ehrlichia chaffensis
6.Species: Borbacin 21-Aug-1998 #text_change 17-Mar-1999
6.A.Cession: JE0219
7.Species: Borbacin 247, 636-643, 1998
7.Fitle: Molecular characterization of a 28kDa surface antigen gene family of the tribe
7.Species number: JE0216; MuID:98321180
7.Species: DNA
7.Reference number: JE0216
7.Species: DNA
7.References: GB:AF062761
7.Species: L286 <RED>7.Species: L286 <RED>7.Spec
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C;Species: Cowdria runniantium (heartwater rickettsia)

C;Species: Cowdria runniantium (heartwater rickettsia)

C;Species: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 08-Oct-1999

C;Accession: 140882; 842827

R;Van Vliet, A.H.; Jongejan, F.; van Kleef, M.; van der Zeijst, B.A.

A;Title: Molecular cloning, sequence analysis, and expression of the gene encoding the

A;Reference number: 140882; MUID:94178956

A;Accession: 140882

A;Status: preliminary; translated from GB/EMBE/DDBJ

A;Molecule type: DNA

A;Residues: 1-204 «RES>

A;Conetics: Publ:X74250; NID:9454266; PIDN:CAA52309.1; PID:9454267

C;Genetics: A;Gene: mapl
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Pred. No. 0.1;
4; Mismatches 2; Indel's
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Pred. No. 1.5;
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0.22;
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Pred. No. 0.22
4; Mismatches
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64.3%;
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50.0%;
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Best Local Similarity 60.0%;
Matches 9; Conservative
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Best Local Similarity 64.3
Matches 9; Conservative
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59 NTTVGVFGLKQNWDG 73
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| |::||::||
63 TKAVFGLKKDWDGV 76
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Best Local Similarity
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Absorription: The sequence of C. elegans cosmid C54G7.

A; Reference number: 218416

A; Reference number: 21840

A; Reference number: 21851

A; Reference number: 21
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C;Species: Caenorhabditis elegans
C;Decies: Caenorhabditis elegans
C;Accession: T2393
C;Accession: T2393
R;Dobson, R.
submitted to the EMBL Data Library, October 1996
A;Reference number: 219819
A;Accession: T2393
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross references: EMBL:281105; PIDN:CAB03219.1; GSPDB:GN00019; CESP:R05D7.4
A;Estidus: 1-299 <WIL>
A;Estidus: 1-299 CVIL>
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C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 15-Sep-2000
C;Accession: T15839
R;Du, Z.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 43; DB;
Pred. No. 34;
1; Mismatches
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Pred. No. 18;
4; Mismatches
ed. No. 7;
Mismatches
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C;Species: Neurospora crassa
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A;Gene: CESP:R05D7.4
A:Map position: 1
A:Introns: 29/3; 122/1; 162/1; 231/2; 268/3
C;Superfamily: tropinesterase
     Pred.
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Best Local Similarity 47.4%;
Matches 9; Conservative
56.2%;
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351 TVATYTLSAVWHGVS 365
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C. Species: Helicobacter pylori
C. Saccession, 5.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weldman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A.Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A.Reference number: A64520; MUD:97394467
A.Accession: G64558
A.Accession: G64558
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
A.Residues: 1-122 <TOM>A.Residues: 1-122 <TOM A.Residues: 1-122 <TOM A.Residues: 1
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A; Title: The complete genome sequence of the lactic acid bacterium.
A; Reference number: A86625
A; Reference number: A86625
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1649
A; Residues: 1-1649
A; Residues: GB: AE005176; NID: g12724583; PIDN: AAK05677.1; GSPDB: GN00146
A; Reperimental source: strain IL1403
A; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Gen
                                                                                                                                   C. Accession: JE0221
R. Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Biochem. Biochys. Res. Commun. 247, 636-643, 1998
A;Title: Molecular characterization of a 28kDa surface antigen gene family of the tribe
A;Reference number: JE0216; MUID:98321180
A;Accession: JE0221
A;Accession: JE0221
A;Accession: JE0221
A;Residues: 1-133 < RED>
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                                                    C;Species: Ehrlichia canis
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 21-Jul-2000
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Pred. No. 3;
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Pred. No.
28k surface antigen 2 - Ehrlichia canis
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1601 SPTTGTFKLNQNWNSTS 1617
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Matches 7; Conservative
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62 TTVVYGLKENWAG 74
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Length 1465; Indels

Score 42.5; DB 2; Pred. No. 1.3e+02; 1; Mismatches 0;

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R;Janetzky, B.; Lehle, L.
J. Biol. Chem. 267, 19798-19805, 1992
A;Titler Ty4, a new retrotransposon from Saccharomyces cerevisiae, flanked by tau-ele A; Reference number: S31261; MUID:93015829
A;Reference number: S31262
A;Residues: L1465 <JANN
A;Residues: 1-1465 <JANN
A;Residues: 1-1465 <JANN
A;Residues: Tetrotransposon Ty4
C;Genetics:
A;Mobile element: retrotransposon Ty4
C;Superfamily: TyB protein
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ilarity 69.2%;
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Best Local Similarity
Matches 9; Conserv
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Job time:
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C; Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jul-2000
C; Accession: S04255; A23941; E31277
R; Geever, R.F.; Huiet L.; Baum, J.A.; Tyler, B.M.; Patel, V.B.; Rutledge, B.J.; Case, M. A: Tile: DAS sequence, organization and requlation of the qa gene cluster of Neurospora A; Reference number: S04250; MUID:89293848
A; Molecule type: DNA
A; Residues: 1-918 CGIL>
A; Molecule type: DNA
A; Reference number: A33941; MUID:86205901
A; Molecule type: DNA
A; Reference number: A33941; MUID:86205901
A; Molecule type: DNA
A; Residues: 1-904, 'R', 906, 'R', 908-918 CGIL2>
A; Residues: 1-904, 'R', 906, 'R', 908-918 CGIL2>
A; Cross references: GB:M13208; NID:9168869; PIDN:AAA33612.1; PID:9168870
A; Residues: 1-904, 'R', 906, 'R', 908-918 CGIL2>
A; Cross references: GB:M13208; NID:9168869; PIDN:AAA33612.1; PID:9168870
A; Note: this sequence has been revised in reference S04250
C; Genetics:
A; Gene: qa: 1s
A; Introns: 76/1
C; Superfamily: shikimate dehydrogenase homology C; Reywords: DNA binding; repressor; transcription requiation
F; 649-877/Domain: shikimate dehydrogenase homology <
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C. Species: Helicobacter pylori
C. Species: Leb-1999
C. Saccession: G71838
C. Accession: G71838
B. Alm, R. A., Ling, L. S. L.; Moir, D. T.; King, B. L.; Brown, E. D.; Dolg, P. C.; Smith, D. R.;
I Ives, C.; Gibson, R.; Merberg, D.; Mills, S. D.; Jiang, Q.; Taylor, D. E.; Vovis, G. F.;
Nature: 397, 176-180, 1999
A. Reference number: A71800; MUD: 99120557
A. Reference number: A71800; MUD: 99120557
A. Status: preliminary
A. Molecule type: DNA
A. Residues: 1-328 <ARN>
A. Residues: 1-328 <ARN>
A. Residues: 1-328 <ARN>
A. Residues: Strain J99
A. Stroperimental source: strain J99
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Pred. No. 67;
1; Mismatches 5; Indels
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Best Local Similarity 57.1%;
Matches 8; Conservative 1
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TyB protein - yeast (Saccharomyces cerevisiae) retrotransposon Ty4 (fragment)
C;Species: Saccharomyces cerevisiae
C;Date: 18-Jun-1993 #sequence_revision 25-Apr-1997 #text_change 26-May-2000
C;Accession: S31262

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bacillus su
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                            100059 seqs, 36664827 residues
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YF02_MYCPN

YF01_MYCPN

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    protein search, using sw model

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clostridium mycoplasma xanthomonas pasteurella caprine art alteromonas photobacter saccharomyc

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Score 46; DB 1; Length 1034; Pred. No. 11; L; Mismatches 7; Indels

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MATAJIMB N., HILOSAWA M., SUGIULA M., SASAMOLO S., KIMURA T.,

MASOUCHI T., MATESUNO A., MURAKI A., NAKAZAKI N., NARUO K., Okumura S.,

A Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,

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P74290;
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30-MAY-2000 (Rel. 39, Last sequence update)
20-AGG-2001 (Rel. 40) Last annotation update)
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Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
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InterPro: IPR001449, PBEcase.
Pfan: PF00311; PEECase; 3.
PRIMTS. PR00130; PEPCAREXLASE.
PROSITE; PS00781; PEPCASE_2; 1.
PROSITE; PS00781; PEPCASE_1; 1.
PROSITE; Carbon dioxide fixation; Allosteric enzyme; Tricarboxylic acid cycle; Complete proteome.
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-S286 / AB972;
Pearson D., Bowman S., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1995) to the EMBL/Genbank/DDBJ databases
--- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
--- SIMILARITY: BELONGS TO THE MALOR FACILITATOR FAMILY (ALSO KNOWN AS THE DRUG RESISTANCE TRANSLOCASE FAMILY). DHA12 SUBFAMILY.
                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fundi, Ascomycota; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                  003263;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
HYPOTHETICAL 59.6 KDA PROTEIN IN DSK2-CAT8 INTERGENIC REGION.
WRR279G OR YM8021.05C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transport; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 AA
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Pred. No. 8.4;
; Mismatches
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                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.18;
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2 NLAVPAFGLSTNWSGN 17
                                                                                                                 STANDARD;
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TRANSMEM 62 8:
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Best Local Similarity
Matches 7; Conserva
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540 AA;
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GVPM_HALME
ID GVPM_HA
AC Q02238
                                                                        RESULT 3
YM8M_YEAST
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RESULT 7
YC05_MYCPN
ID YC05_MYCPN
AC 275571,
DT 20-AUG-2001 (1)
DT 20-AUG-2001 (1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pneumoniae.
                                                                                                                                                                                                                                                                                           YB01_MYCPN
P75568;
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                                                               Halobacterium mediterranei (Haloferax mediterranei).
Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae; Haloferax.
NCBI_TaxID=2252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                 ij.
                                                                                                                                                                                    J. Mol. Biol. 227:586-592(1992).
-!- FUNCTION: COULD BE IMPORTANT FOR THE SHAPE DETERMINATION OF THE
                                                                                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDIATE—99301102; PubMed=1404376;
MEDIATE—9931102; PubMed=1404376;
Englert C., Krueger K., Offiner S., Pfeifer F.;
Three different but related gene clusters encoding gas vesicles
                                                                                                                                                                                                                             -!- SIMILARITY: HIGH, TO GVPJ AND TO GAS VESICLE PROTEINS TYPE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-ATCC 20342 / M129;
MEDLINE-97105885; Pubmed-8948633;
Himmelreaich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
Herrmann R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43; DB 1; Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           86 AA; 9355 MW; AB522F20C6F63666 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 24:4420-4449(1996).
-!- SIMILARITY: BELONGS TO THE ADHESIN P1 FAMILY.
             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL PROTEIN MPN502 (P02_ORF422V).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       422 AA
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5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                PIR, S28126; S28126.
InterPro; IRR000638; Gas_vesicle.
Pfam; PF00741; Gas_vesicle. 1.
ProDom; PD003598; Gas_vesicle; 1.
PROSITE; PS00234; GAS_VESICLE__1; 1.
PROSITE; PS00669; GAS_VESICLE__1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycoplasma pneumoniae.
01-JUL-1993 (Rel. 26,
01-JUL-1993 (Rel. 26,
01-JUL-1993 (Rel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserv.
                                                                                                                                                                           halophilic archaea.
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                                                                                                                                                                                                                GAS VESICLE.
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                                      GVPM PROTEIN.
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P75285:
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                                                                                                                                                                                                                                                                                                                                                            Score 43; DB 1; Length 422;
Pred. No. 14;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.2%; Score 43; DB 1; Length 428; 70.0%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acids Res. 24:4420-4449(1996).
-! SIMILARITY: BELONGS TO THE ADHESIN PI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                            Hypothetical protein; Complete proteome.
SEQUENCE 422 AA; 46141 MW; 03BE7D381C7CC298 CRC64;
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SEQUENCE 428 AA; 46908 MW; 991143BEF683A261 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
MPN101 OR MP053.
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(Rel. 40, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; Pubmed-8948633;
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70.0%;
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Best Local Similarity 70.0
Matches 7; Conservative
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141 NTTIGAYGLK 150
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Matches 7; Conserv
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protein.
648 AA;
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                                Envelope | SEQUENCE
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GLSF_PORPU
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I SIMILARITY: BELONGS TO THE ADHESIN PI FAMILY.

I SIMILARITY: BELONGS TO THE ADHESIN PI FAMILY.

I SIMILARITY: BELONGS TO THE ADHESIN PI FAMILY.

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                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete sequence analysis of the genome of the bacterium Mycoplasma
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MEDLINE-881660044; PubMed-377997; Carton J., Strassman J.,

METAGE B., Metzger S., Romantschuk M., Carton J., Strassman J.,

Gottlieb P., Metzger S., Romantschuk M., Carton J., Strassman J.,

Mincled D.H., Kalkkinen N., Mindich L.;

"Nuclectide sequence of the mindich associated proteins.";

"Incleding 163:183-190(1988).

"Incledy 163:183-190(1988).
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0
                                                                                                Mycoplasma pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
NCBL_TaxTD=2104;
                                                                                                                                                                                                                                                LEDUENCE FROM N.A.
STRAIN-ATCC 2942 / M129;
STRAIN-E97105885; PubMed-8948633;
Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43; DB 1; Length 438;
Pred. No. 14;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE000060; AAB96274.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 438 AA; 47925 MW; D6CB89515576AD7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VP3_BPPH6 STANDARD; PRT; 648 AA.
VP3_BPPH6 STANDARD; PRT; 648 AA.
D1129;
01-JU1-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 13, Last sequence update)
01-JAN-1990 (Rel. 13, Last annotation update)
P3 PROTEIN.
P3 Bacteriophage phi-6.
VIRUSES; GSRAM viruses; Cystoviridae; Cystovirus.
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL PROTEIN MPN205 (GT9_ORF438V).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M17462; AAA68485.1; -.
PIR; C28648; P3BPF6.
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                                                                MPN205 OR MP626
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10 V93_BPPH6
10 V93_BPH6
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Chloroplast.
Ebkaryota: Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
NCBL_Tax1b=2787;
                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=AVONPORT;
Strain M.E., Munholland J.;
"Complete nucleotide sequence of the Porphyra purpurea chloroplast genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0c7-1996 (Rel. 34, Created)
01-0c7-1996 (Rel. 34, Last sequence update)
20-AGG-2001 (Rel. 40, Last annotation update)
FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE (EC 1.4.7.1) (FD-GOGAT).
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                                                                                                    Score 43; DB 1; Length 648;
Pred. No. 22;
7; Mismatches 1; Indels
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B188DFE02ACC54E3 CRC64;
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Pred. No. 64;
1; Mismatches
69178 MW;
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                                                                                        Query Match
Best Local Similarity 41.2%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                181 IFGWYVKMDWEGSAVAD 197
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39.1%;
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Best Local Similarity
9; Conserve
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RESULT 11 ATNA_DROME

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Melnick L., Sherman F.;
"The gene clusters ARC and COR on chromosomes 5 and 10, respectively, of Saccharomyces cerevisiae share a common ancestry.";
of Saccharomyces cerevisiae share a common ancestry.";
J. Mol. Biol. 233:372-386(1993).
                                                                                                                                                                                                                                                                                                                                      Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R., Avalies E., Berno A., Brennan T., Carpenter T., Chen E., Cherry J.M. Berno A., Brennan T., Carpenter T., Chen E., Cherry J.M. Grund E., Duncan M., Giraman E., Hartzell G., Hunicke-Smith S., Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Mossedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.; Submitted (BEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                    Mulligan J.T., Dietrich F.S., Hennessey K.M., Sehl P., Komp C., Wel Y., Taylor P., Nakahara K., Roberts D., Davis R.W.; Submitted (FEB-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 347;
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A -> R (IN REF. 3).
S -> C (IN REF. 3).
1E8AFB862C4BB328 CRC64;
                                                                   01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
UTR2 PROTEIN (UNKNOWN TRANSCRIPT 2 PROTEIN).
UTR2 OR YELO40W OR SYGP-ORF18.
                  347 AA.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, L22173; AAA34941.1;
EMBL, S65964; AAD13975.1;
EMBL, S65964; AAD13975.1;
PIR, S30839; S30839.
HSSP; P23904; IAJO.
SGD, S000706; UTR2.
InterPro; IPR000757; Glyco_hydro_16.
Pfam: PF00722; Glyco_hydro_16.
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                    PRT;
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                                                      27, Created)
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                    STANDARD;
                                                  01-OCT-1993 (Rel. 27, 01-OCT-1994 (Rel. 30,
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347 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                   NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=B-6441
                    UTR2_YEAST
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                                   P32623;
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UTR2_YEAST
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TRANSPROME 91 STANDARD:

DATA DROWE 91 STANDARD:

DATA OF ANGE 2010 (Meal - 40) Last sequence update)

DATA MIC 2010 (Meal - 40) Last sequence update)

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Gaps

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7; Indels

Mismatches

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Matches

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hes 9; Conservative
3 TVGVFGLKQNWDGSAISN 20
| | | | | | | | |
148 TIAWSGGEINWDASDISN 165

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39.3%;
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Subfilist; BG10033; yyaR.
InterPro; IPR000182; Acctyltr.
Pfam; PF00583; Acctyltransf;
Hypothetical protein; Complet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115604
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Best Local Similarity 33.3%;
Matches 6; Conservative
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Best Local Similarity
Matches 5; Conserv
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                                    YYAR_BACSU
P37506;
                             CONFLICT
CON
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ATP (BY SIMILARITY).
MISSING (IN ISOFORM 3 N.
MISATURG (IN ISOFORM 3 N.
MISALIWERPREPREVENCY S.
ATABLIMERREPREPREVENCY S.
AL N. IN REF. 1).
K -> R (IN REF. 1).
MISSING (IN REF. 1).
MISSING (IN REF. 1).
                             SEQUENCE OF 400-524 FROM N.A.

MEDLINE-90092469; PubMed=257235;

Varadi A., Gilmore-Heber M., Benz E.J. Jr.;

Varadi A., Gilmore-Heber M., Benz E.J. Jr.;

Amplification of the phosphorylation site-ATP-binding site cDNA fragment of the Na+,K(+)-ATPase and the Ca2(+)-ATPase of Drosophila FEBS Lett. 258:203-207(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transport; Transmembrane;
ng; Alternative splicing.
POTENTIAL.
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
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EMBL; AF044934; AAC05260.1; --
EMBL; AE003732; AAF55825.2; ---
EMBL; AE003732; AAF55827.2; ---
EMBL; AE003732; AAF55827.2; ---
EMBL; AE003732; AAF55827.2; ---
EMBL; AE00372; AAF55827.2; ---
EMBL; AE00372; AAF55827.2; ---
EMBL; GS767; AAB01189.1; ---
INTERFO; EMBONO5221; ALP-alpha.
INTERFO; IPRO01221; ALP-alpha.
INTERFO; IPRO01221; ALP-alpha.
INTERFO; IPRO01221; ALP-alpha.
INTERFO; IPRO0124; AYPEASE.
INTERFO; IPRO0125; AYPEASE.
INTERFO; IPRO0129; AYPEASE.
INTERFO; IPRO0139; CATAPASE.
INTERFO; PRO0119; CATAPASE.
INTERFO; PRO0119; CATAPASE.
INTERFO; PRO0119; AYPEASE.
INTERFO; PRO0119; AYPEASE.
INTERFO; PRO0119; AYPEASE.
INTERFO; PRO0119; AYPEASE.
INTERFO; PROO119; AYPEASE.
INTERFO; PROO119; AYPEASE.
INTERFO; PROO119; AYPEASE.
INTERFO; PROO119; AYPEASE.
INTERFO; PROFINIAL
INTERFORME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=168;
MEDLIN=-96051385; PubMed-7584024;
MEDLINE-96051385; PubMed-7584024;
Ogaswara N., Nakai S., Yoshikawa H.;
Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chromosome containing the replication origin.";
DNA Res. 1:1-14(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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KN -> ED (IN REF. 1).

I -> V (IN REF. 1).

I -> V (IN REF. 1).

E -> G (IN REF. 2).

LT -> PS (IN REF. 2).

VW -> VL (IN REF. 1).

VW -> LE (IN REF. 1).

VW -> LE (IN REF. 1).

RIPADI -> LIPLVY (IN REF. 1).

RIPADI -> LIPLVY (IN REF. 1).

GTA -> ALP (IN REF. 1).

F -> S (IN REF. 1).

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E -> D (IN REF. 1).

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E -> D (IN REF. 1).
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01-00T-1994 (Rel. 30, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 20.4 KDA PROTEIN IN COTF-TETB INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42; DB 1; Length 1041; Pred. No. 52; '; Mismatches 3; Indels
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Pred. No. 12;
5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  al protein; Complete proteome.
173 AA: 20393 MW; 0FB09B59F6A056BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria: Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
NCBI_TAXID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 173 AA.
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Thu Mar 14 10:13:35 2002

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JHP1298
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025956;
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                                                                                                                                                                                                                                                                                                                 Loeffelhardt W., Stirewalt V.L., Michalowski C.B., Annarella M., Earley J.Y., Schluchter W.M., Chung S., Newmann-Spallart C., Steiner J.M., Jakowitsch J., Bohnert H.J., Bryant D.A.; The complete sequence of the cyanollete genome of Cyanophora paradoxa: the genetic complexity of a primitive plastid."; (In) Schenk H.B.A., Herrmann R., Jeon K.W., Mueller N.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                       "Nucleotide sequence of the cyanelle DNA from Cyanophora paradoxa."; Plant Mol. Biol. Rep. 13:327-332(1995).
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotism and Symbiosis, pp.40-48, Springer-Verlag, Heidelberg
                                                                                                                                                                                                                                  Stirewalt V.L., Michalowski C.B., Loeffelhardt W., Bohnert H.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SIMILARITY: BELONGS TO THE S2P FAMILY OF RIBOSOMAL PROTEINS.
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                                                                                                                                                                 Eukaryota; Glaucocystophyceae; Cyanophoraceae; Cyanophora.
NCBI_TaxID=2762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 233;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ribosomal protein; Cyanelle. – SEQUENCE 233 Aa; 26198 MW; 06D3BAD7DA9A883F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38.3%; Score 41; DB 1; 36.8%; Pred. No. 16;
                                                                                           01-FEB-1996 (Rel. 33, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CYANELLE 30S RIBOSOMAL PROTEIN S2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mendel, 7923; GYAPAJTPS2;1.
InterPro: IPR001865; Ribosomal_S2.
Pfam: PR00318; Ribosomal_S2.
PRUMS: PR00395; RIBOSOMALS2.
PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
PROSITE; PS00963; RIBOSOMAL_S2_2; 1.
                                                          PRT;
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                                                                                 01-FEB-1996 (Rel. 33, Created)
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85 TRCGAFYINQRWLGGTLTN 103
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74 NNCIGRIKIRSNWNGYAL 91
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                                                                                                                                                                                                                     STRAIN-LB555 / PRINGSHEIM;
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                                                           STANDARD;
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                                                                                                                                              Cyanophora paradoxa.
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                         RR2_CYAPA
P48132;
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                                   RESULT 13
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BIOB_HELPJ
                                               RR2_CYAPA
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MEDLINE-97394467; PubMed-9252185;
MEDLINE-97394467; PubMed-9252185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Teleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                        Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
-!- CATALYTIC ACTIVITY: DETHIOBIOTIN + (s) = BIOTIN.
-!- PATHWAY: LAST STEP IN BIOTIN BIOSYNTHESIS PATHWAY.
-!- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES FAMILY.
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Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter.
Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE001553; AAD06876.1; -
EMBL; AE001553; AAD06867.1; -
Interpro; IPR002684; Biotin_synth.
Pfan; PF01792; Biotin_synth;
Biotin biosynthesis; Iron-sulfur; Transferase; Complete proteome.
METAL 17 IRON-SULEUR (POTENTIAL).
AMETAL 21 21 IRON-SULEUR (POTENTIAL).
24 24 24 24 24 24 24 24 3A07177865AFAFIB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
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15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE).
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4; Mismatches
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                                                                                                                                                                                                                      MEDLINE=99120557; PubMed=9923682;
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Best Local Similarity
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                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                             NCBI_TaxID=85963;
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Venter J.C.;
"The complete genome sequence of the gastric pathogen Helicobacter
                        pylori.";

Mature 388:539-547(1997)

-!- CATALYTIC ACTIVITY: DETHIOBIOTIN + (S) = BIOTIN

-!- CATALYTIC ACTIVITY: DETHIOBIOTIN BIOSYNTHESIS PATHWAY.

-!- PATHWAY: LAST STEP IN BIOTIN BIOSYNTHESIS PATHWAY.

-!- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
FAMILY.
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Search completed: March 14, 2002, 09:24:50 Job time: 906 sec

|:||| ::|: | 157 GIFGLNESWE 166 5 GVFGLKQNWD 14

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0; Gaps

Query Match

38.3%; Score 41; DB 1; Length 282;
Best Local Similarity 50.0%; Pred. No. 19;
Matches 5; Conservative 4; Mismatches 1; Indels

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092gjl ehrlichia c
09f475 ehrlichia c
08f360 ehrlichia c
05f474 ehrlichia c
052106 ehrlichia c
052104 ehrlichia c
09amf6 cowdria sp.
09af21 cowdria rum
09af21 cowdria rum
09af22 brachydanio
09aeu3 cowdria rum
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caenorhabdi
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Alleman A.R.;
Molecular characterization of a 28 kDa surface antigen gene family of the tribe Enrlichiae.";
Biochem. Biophys. Res. Commun. 247:636-643(1998).
EMBL; AF062761; AAC26716.1;
Interpro: IPR002566; Surface_Ag_msp4.
Pfam; PF01617; Surface_Ag_msp4.
NON_TER
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                                                                                                                                                                                                                                                                           085358 PRELIMINARY; PRT; 276 AA.
085358;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
28 KDA MAJOR SURFACE ANTIGEN-5 (FRAGMENT).
ENTILICHIA CATAFFERSIS, alpha subdivision; Rickettsiales; Rickettsiaceae; Ehrlichieae; Ehrlichieae; Ehrlichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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Pred. No. 1.4e-09;
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        Q9F475
Q9F474
Q9F474
O52106
Q9AMF6
Q46327
Q90F22
Q9AEU3
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095641
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046333
096333
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STRAIN=ARKANSAS;
MEDLINE=98321180; Pubmed=9647746;
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                          Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
 NON_TER
SEQUENCE
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085358
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09587 ehrlichia c
085817 ehrlichia c
085816 ehrlichia c
08510 ehrlichia c
052107 ehrlichia c
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095103 ehrlichia c
096803 ehrlichia c
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097803 ehrlichia c
097804 ehrlichia c
097805 ehrlichia c
                                                                 (without alignments)
28.301 Million cell updates/sec
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                                                        March 14, 2002, 09:24:09; Search time 103.37 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                  473505 seqs, 146272329 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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                                                                                         US-09-765-739A-3
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1 NTTVGVFGLKQNWDGSAISN
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sp_bacteria:*
sp_fung1:*
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sp_virus:*
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246 AA.

PRT;

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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-99175287; Pubbled=10074538;
Yu X.J. McBride J.W. Walker D.H.;
Yu X.J. McBride J.W. Walker D.H.;
'Genetic diversity of the 20-kilodalton outer membrane protein gene in human isolates of Ehrlichia chaffeensis.";
J. Clin. Microbiol. 37:1137-1143(1999).
Interpro; IPRO01702; Gram_neg_porin.
Interpro; IPRO02566; Surface_Ag_msp4.
Fam: PF01617; Surface_Ag_msp4.
Fam: PF01617; Surface_Ag_msp4.
PRINTS; PR00182; ECOLNEIPORIN.
NON_TER
SEQUENCE 246 AA; 26884 MW; C9776392C5129A2F CRC64;
                                                                                                                                                                                                                                                                                                        Ehrlichia chaffeensis.
Bacteria: Proteobacteria: alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
NCBI_TaxID=945;
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82.2%; Score 88; DB 2; Length 246
Best Local Similarity 88.9%; Pred. No. 1.6e-06;
Matches 16; Conservative 1; Mismatches 1; Indels
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01.-UNAY-2001 (TrEMBLrel. 17, Last annotation update)
00.-UNBRANE PROTEIN P28 PRECURSOR (FRAGMENT).
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SEQUENCE FROM N.A.
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EMBL, AF062761; AAC26720.1; Difference Ag_msp4.

Fight, PF01617; Surface_Ag_msp4.

SEQUENCE 280 AA; 30743 MW; FBBB41DAF08EE4DC CRC64;
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SEQUENCE FROM N.A.
MEDLINE-21153566; PubMed-11254561;
Ohashi N., Rikihisa Y., Unver A.;
Ohashi N., Rikihisa Y., Unver A.;
Maalysis of Transcriptionally Active Gene Clusters of Major Outer Membrane Protein Multigene Family in Ehrlichia canis and E.
chaffeensis."; 69:2083-2091(2001).
EMBL; U72291; ARK286731; --
SEQUENCE 281 AA; 30343 MW; A99E5F7C4459AA9A CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 07, Last annotation update)
01-NON-2001 (TrEMBLREL. 17, Last annotation update)
28 KDA MAJOR SURFACE ANTIGEN-4.
Ehrlichia chaffeensis.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
RICKettsiaceae; Ehrlichieae; Ehrlichia.
                                                                                                                                                                    Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
NCBL_TaxID=945;
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Pred. No. 1.5e-09;
Mismatches 0; Indels
01.JUN-2001 (TrEMBLrel. 17, Last sequence update)
1-JUN-2001 (TrEMBLRel. 17, Last annotation update)
MAJOR OUTER MEMBRANE PROPERN P28.
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Best Local Similarity 100.0%; Pred. No. 1.5
Matches 20; Conservative 0; Mismatches
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Best Local Similarity
Matches 16; Conserv
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NCBI_TaxID=945;
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Pred. No. 1.9e-06;
1; Mismatches 1; Indels
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Submitted (Jul-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF07734; AAC31547.1;
-InterPro: IPR002566; Surface_Ag_msp4.
Pfam; PF01617; Surface_Ag_2; 1.
SEQUENCE 276 AA; 30027 MW; 2FD3698FCF1F60BE CRC64;
                                                                                                                                                                                   01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
00TER MEMBRANE PROTEIN P28 PRECURSOR.
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29 NTTAGVFGLKQDWDGSAI 46
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Best Local Similarity 88.9
Matches 16; Conservative
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STRAIN-ARKANSAS;
MEDLINE-98084465; PubWed-9423849;
Ohashi N., Zhi N., Zhang Y., Rikihisa Y.;
Ohashi N., Zhi N., Zhang Y., Rikihisa Y.;
Immunodominant major outer membrane proteins of Ehrlichia chaffeensis are encoded by a polymorphic multigene family.";
Infect. Immun. 66:132-139(1998).
EMBL: 972291; AAC02940.1;
EMBL: 972291; AAC02040.1;
Pfam; PPO1617; Surface_Ag_msp4.
Pfam; PPO1617; Surface_Ag_1.1.
SEQUENCE 280 AA; 30731 MW; CCAA6C34E2AF393E CRC64;
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                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McBride J.W., Yu X.J., Walker D.H.; "A conserved, transcriptionally active p28 multigene locus of
                           Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
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Rickettsiaceae; Ehrlichieae; Ehrlichia.
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Gene 24:245-251(2000).
EMBL: AF078525:35 AC08667.1; -.
EMBL: AF07852744; AAG14362.1; -.
InterPro: IPR002566; Surface_Ag_msp4.
Pfam; PF01617; Surface_Ag_2.1.
EQUENCE 288 AA, 31590 MW; 86DCAECB88E9BF5E CRC64;
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PROTEIN (P28-8)
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84.2%; Pred. No. 1.9e-06;
ive 1; Mismatches 2;
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MEDLINE-20432107; PubMed-10974556;
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Matches 16; Conservative
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Rickettsiaceae; Ehrlichieae; Ehrlichia.
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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
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"Ehrlichia chaffeensis 28 kDa outer membrane protein.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
BMBL; AR07732; AAC31545.1; --
Inter: PR002566; Surface_Ag_msp4.
Pfam; PF01617; Surface_Ag_2; 1.
SEQUENCE 280 AA; 30277 MW; 91C54AC78507A63F CRC64;
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"Ehrlichia chaffeensis 28 kDa outer membrane protein.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AR077733; AAC31546-1;
Interpro: IRR002566; Surface_Ag_msp4.
Pfam; PF01617; Surface_Ag_2; 1.
SEQUENCE 280 AA; 30304 MW; 91C54AC7851B77F2 CRC64;
                                              01-JUN-2001 (TIEMBLIEL 08, Last sequence update) 01-JUN-2001 (TIEMBLIEL 17, Last annotation update) OUTER MEMBRANE PROTEIN P28 PRECURSOR.
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1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-EMBRANE PROTEIN P28 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                        Score 88; DB 2; Pred. No. 1.9e-06;
               280 AA
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80.0%;
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             PRELIMINARY;
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Best Local Similarity
Matches 16; Conserv
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                             NCBI_TaxID=945;
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                                                                                                                                                                                         STRAIN=91HE17
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01-JUN-1998
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OMP-1F.
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01-NOV-1998
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1 NTTVGVFGLKQNWDGSAIS 19
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SEQUENCE FROM N.A.
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052105
ID 052105
AC 052105;
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STRAIN-JAKE,
MEDLINE-9524757; PubMed-10225842;
MEDLINE-95247757; Walker D.H.;
MOBIGE J.W., Yu, Xj, Walker D.H.;
Molecular cloning of the gene for a conserved major immunoreactive
Molecular cloning of the gene for a conserved major immunoreactive
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MEDLINE-20482107; PubMed-10974556;
MEDLINE-20423107; Walker D.H.;
"A conserved, transcriptionally active p28 multigene locus of Enrichia canis.";
Gene 254:245-252(2000).
EMBL; AF087744; AAG14361.1; -
EMBL; AF087745; AAG24361.1; -
FIGHEPPO; IPRO02566; Sufface_A_msp4.
Pfam; PF01017; Surface_A_L.1.
SEQUENCE 280 AA; 30762 MW; BE284A4B94FE3123 CRC64;
                                                                                                                                                                                                                                                   Ehrlichia canis.
abacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
NCBL_TAXID-944;
                    Length 288;
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Rickettsiaceae; Bhrlichleae; Bhrlichla.
NCBL_TaxID=944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 74.8%; Score 80; DB 2; Length 280; Best Local Similarity 70.0%; Pred. No. 38e-05; Matches 14; Conservative 3; Mismatches 3; Indels
               Query Match 76.6%; Score 82; DB 2; Length 28E Best Local Similarity 70.0%; Pred. No. 1.9e-05; Matches 14; Conservative 3; Mismatches 3; Indels
                                                                                                                                                    O9F473 PRELIMINARY; PRT; 280 AA.

09F473;

01-MAR-2001 (TrEMBLrel. 16, Created)

01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

10-TUD-2001 (TrEMBLrel. 17, Last annotation update)

P28-6.
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01.5070-2001 (TrEMBLrel. 17, Last sequence update)
01.50701 (TrEMBLrel. 17, Last annotation update)
MAJOR OUTER MEMBRANE PROFEIN P30-2.
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Clin. Diagn. Lab. Immunol. 6:392-399(1999).
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STRAIN-OKLAHOMA;
MEDLINE-98371112; PubMed-9705412;
                                                                  1 NTTVGVFGLKQNWDGSAISN 20
                                                                                    60 NTTTGVFGLKQDWDGATIKD 79
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Q9F473
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MEDLIN-B-98321180; PubMed-9647746;
Reddy G.R., Sulsona C.R., Barbet A.F., Mahan S.M., Burridge M.J.,
Alleman A.R.;
"Molecular characterization of a 28 kDa surface antigen gene family of
the tribe Enrichiae.";
Blochem. Biochem. Bi
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SEQUENCE FROM N.A.
STRAIN-ARKANSAS;
WEDLINE-98084465; PubMed-9423849;
Ohashi N., Zhi N., Zhang Y., Rikkhisa Y.;
Immunodominant major outer membrane proteins of Ehrlichia chaffeensis
are encoded by a polymorphic multigene family.";
Infect. Immun. 66:132-139(1998).
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PREALINE-21133566; PubMed=11254561;

Chashi N., Rikihisa Y., Unver A.;

Analysis of Transcriptionally Active Gene Clusters of Major Outer

Membrane Protein Multigene Family in Ehrlichia canis and E.

chaffeensis."; po 22083-2091 (2001).

EMBL; ARVOR9553; AARX2699.1; --

SEQUENCE 280 AA; 30803 MW; 27238BEIC7E68A91 CRC64;
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Ohashi N., Unver A., Zhi N., Rikihisa Y.;
Cloung and characterization of multigenese encoding the immunodominant 30-kilodalton major outer membrane proteins Britichia canis and application of the recombinant protein serodiagnosis."
J. Clin. Microbiol. 36:2671-2680(1998).
SEQUENCE FROM N.A.
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Ehrlichia chaffeensis.
Ehrlichia stateria: alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
NCBI_TaxID=945;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Search completed: March 14, 2002, 09:24:09 Job time: 980 sec
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                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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RESULT 15
               09R8A7
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MCBride J.W., Yu X.J., Walker D.H.;
"Molecular cloning of a conserved major immunoreactive 28-kilodalton protein gene from a polymorphic multiple gene family of Ehrlichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McBride J.W., Yu X.J., Walker D.H.; "Modecular cloning of a conserved major immunoreactive 28-kilodalton protein gene from a polymorphic multiple gene family of Ehrlichia canis.";
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 17, Last annotation update)
28 KDA OUTER MEMBRANE PROTEIN (FRAGMENT).
29 LItchia canis.
BACTERIA: Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 13, Last annotation update)
28 KDA OUTER MEMBRANE PROTEIN (FRAGMENT).
Ehrlichia canis.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiacee; Ehrlichiacae; Ehrlichiacae; Ehrlichiacae; Ehrlichiacae;
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                                                                                                                                                                                                                                                                                   canis.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
BMBL; AF082745; AAC64551.1;
InterPro; IPR02566; Surface_Ag_msp4.
Pfam; PF01617; Surface_Ag_2: 1.
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                                         278 AA.
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Best Local Similarity 76.5
Matches 13; Conservative
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Matches 13; Conservative
                                          PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                          Q9R8A9;
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           RESULT 13
Q9R8A9
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STRAIN-DEMON (NORTH CAROLINA);
MACBride J.W., Yu X.J., Walker D.H.;
"Molecular cloning of a conserved major immunoreactive 28-kilodalton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               protein gene from a polymorphic multiple gene family of Ehrlichia
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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
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InterPro; IPR002566; Surface_Ag_msp4. Pfam; PF01617; Surface_Ag_2; 1.
NON_TER 278 278
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                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
28 KDA OUTER MEMBRANE PROTEIN (FRAGMENT).
  PRT;
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Best Local Similarity 76.55
Matches 13, Conservative
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THIS PACE OLANG (USOTO)

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Sequence 17, Application US/08953326
Patent No. 6251872
GENERAL INFORMATION:
APPLICANT: Barbet, Anthony F.
APPLICANT: Ganta, Roman R.
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APPLICANT: Burridge, Michael J.
APPLICANT: Nyika, Aceme
APPLICANT: Rurangirwa, Fred R.
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US-08-953-326-17
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7.427 Million cell updates/sec
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Sequence 4,
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-953-326-18
US-08-953-326-18
US-08-733-230-4
US-08-953-326-4
US-08-953-326-2
US-08-953-326-2
US-08-953-326-2
US-08-953-326-2
US-08-953-326-2
US-08-474-140-11
US-08-474-140-11
US-08-474-545-11
US-08-478-331-11
US-08-478-331-11
US-08-96-77-049-11
US-08-96-77-049-11
US-08-96-77-049-11
US-08-646-360-7
US-08-425-336-7
US-08-425-336-7
US-08-48-1138-7
US-08-48-1138-7
US-08-48-1138-7
US-08-646-360-7
US-08-08-97-765-7
US-08-08-97-765-7
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US-08-08-97-765-7
US-08-08-97-766-7
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                                                                                                                                                                212252 seqs, 22503292 residues
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Maximum Match 100%
Listing first 45 summaries
                                   OM protein - protein search, using sw model
                                                       March 14, 2002, 09:07:40
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                                                                                                                1 NPTVALYGLKQDWNGVSA 18
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98
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APPLICANT: Barbet, Anthony F.
APPLICANT: Ganta, Roman R.
APPLICANT: Applicant: Acceme
APPLICANT: McGuire, Travis_C.
APPLICANT: Murangirwa, Fred R.
APPLICANT: Murangirwa, Fred R.
APPLICANT: Rurangirwa, Fred R.
APPLICANT: Rurangirwa, Fred R.
APPLICANT: Rurangirwa, Fred R.
APPLICANT: Rurangirwa, Fred R.
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of TITLE OF INVENTION: Animals and Humans
TITLE OF INVENTION: Animals and Humans
TITLE OF INVENTION Animals and Humans
FILE REFERENCE: UF-1671.
CURRENT FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/953,326
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 2.0
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330, 7
30, 8
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2; Mismatches 1;
US-08-251-288A-2
US-09-298-819A-2
US-08-3737-716-13
PCT-US93-11703-24
US-08-99-568-15
US-08-99-568-15
US-08-956-998-2
US-08-956-998-2
US-08-956-998-2
US-08-944-868A-39
US-08-944-868A-39
US-08-944-423A-39
US-08-944-423A-39
US-08-944-423A-39
US-08-944-423A-39
US-08-944-423A-39
US-08-944-423A-39
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                                                                                                                                                US-08-369-829A-1
US-08-896-933-32
US-08-989-385-1
US-09-346-237-1
                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                  Séquence 16, Application US/08953326 Patent No. 6251872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Ehrlichia chaffeensis
US-08-953-326-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.8%;
83.3%;
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Best Local Similarity 83.3
Matches 15; Conservative
  6009
6711
3393
3393
6443
6443
6443
6443
6443
  08-953-326-16
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  SEQ ID NO 16
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-08-953-326-4
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1 S-08-953-326-18

1 US-08-953-326-18

1 Sequence 18, Application US/08953326

2 Patent No. 6251872

2 Patent No. 6251872

3 PAPLICANT: Barbet, Anthony F.

APPLICANT: Barbet, Anthony F.

APPLICANT: Goodle.

APPLICANT: Michael J.

APPLICANT: Will and Accement Applicant Nucleic Acid Vaccines Against Rickettsial Diseases of TITLE OF INVENTION: Animals and Humans

TITLE OF INVENTION: Animals and Humans

FILE REFERENCE: UF-167C1

CURRENT APPLICATION NUMBER: US/08/953,326

CURRENT FILING DATE: 1997-10-17

EARLIER APPLICATION NUMBER: 08/953,326

EARLIER APPLICATION NUMBER: 08/953,326

EARLIER APPLICATION NUMBER: 08/953,326

EARLIER PILING DATE: 1997-10-17

EARLIER PRICING DATE: 1996-10-17

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 18

LENGTH: 276

TYPE: Pap.
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APPLICANT: Mahan, Suman M.

TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of TITLE OF INVENTION: Nucleic and Humans
FILE REFERENCE: UF-167C1.
FILE REFERENCE: UF-167C1.
GARLIER APPLICATION NUMBER: 08/953,326
CURRENT FILING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-17
NUMBER OF SEQ ID NOS: 2.0
SEQ ID NOS: 2.0
SEQ ID NO 17
LENGTH: 280
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Pred. No. 0.0069;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 57; DB 4; Length 276;
Pred. No. 0.033;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08733230; Patent No. 6025338; Garneal INFORMATION: APPLICANT: Barbet, Anthony F.
                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Ehrlichia chaffeensis
US-08-953-326-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Ehrlichia chaffeensis
US-08-953-326-18
                                                                                                                                                                                                                                                                                                                                                                                                                          62.2%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 58.2%;
Best Local Similarity 60.0%;
Matches 9; Conservative
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Best Local Similarity 60.0
Matches 9; Conservative
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59 NTTVGVFGLKQNWDG 73
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US-08-733-230-4
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APPLICANT: Gallar, Romain Seddy
APPLICANT: Gallar, Romain Seddy
APPLICANT: Gallar, Romain Seddy
APPLICANT: Willian; Romain Seddy
APPLICANT: Willian; Romain Seddy
APPLICANT: Willian; Sulan, Male
APPLICANT: Sallawanhik & Sallamanhik
STREET: 2431 NW 14 1st Street, Sulte A-1
STREET: 2431 NW 14 1st Street, Sulte A-1
STREET: 2431 NW 14 1st Street, Sulte A-1
STREET: 1241 NW
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GENERAL INFORMATION:
APPLICANT: Barbet, Anthony F.
APPLICANT: Ganta, Roman R.
APPLICANT: Guite, Travis C.
APPLICANT: McGuite, Travis C.
APPLICANT: Burridge, Michael J.
APPLICANT: Nyika, Aceme
APPLICANT: Rurangirwa, Fred R.
APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
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Pred. No. 0.56;
5; Mismatches 2; Indels
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Pred. No. 0.37;
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CURRENT FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/953,326
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1996-10-17
SOFTWARE: PATCHIN VOY: 2.0
                                                                                                                                                                                                                                               FILE REFERENCE: UF-167CI
CURRENT APPLICATION NUMBER: US/08/953,326
CURRENT FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/953,326
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1996-10-17
EARLIER FILING DATE: 1996-10-17
NUMBER OF SEQ ID NOS: 24
SOFFWARE: PatentIn Ver. 2.0
                 Sequence 2, Application US/08953326
Patent No. 6251872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Ehrlichia chaffeensis
US-08-953-326-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Cowdria ruminantium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.0%;
57.1%;
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50.0%;
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Best Local Similarity 57.1
Matches 8; Conservative
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Best Local Similarity 50.0
Matches 7; Conservative
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63 TQTVFGLKKDWDGV 76
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LENGTH: 287
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APPLICANT: Burridge, Michael J.
APPLICANT: Nujka, Acceme
APPLICANT: Rurangirwa, Fred R.
APPLICANT: Rurangirwa, Suman M.
TITLE OF INVENTION: Nucleic Acid Vaccines Against
TITLE OF INVENTION: Rickettsial Diseases and Methods of Use
CORRESPONDENCE ADDRESS:
                                                                                                                                 Score 57; DB 4; Length 280;
Pred. No. 0.034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 51; DB 3; Length 287;
Pred. No. 0.37;
                                                                                                                                                                         2; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURREW APPLICATION DATR:
APPLICATION NUMBER: US/08/733,230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
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                                                                                                                                                                                                                                                                                               RESULT 6
US-08-733-230-2
; Sequence 2, Application US/08733230
; Patent No. 6025338
; GENERAL INFORMATION:
; APPLICANT: Barbet, Anthony F.
; Patent No. 7 Travis C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: WhitLock, Ted W.
REGISTRATION NUMBER: 36.965
REFERENCE/DOCKET NUMBER: UF-1
TELECOMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEPHONE: 352-375-800
                                                     ORGANISM: Ehrlichia chaffeensis
US-08-953-326-4
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                                                                                                                                 58.2%;
60.0%;
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57.1%;
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                                                                                                                                                     Best_Local Similarity 60.0
Matches 9; Conservative
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60 NTTVGVFGLKQNWDG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-733-230-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 514
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63 TQTVFGLKKDWDGV 76
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Best Local Similarity
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SEQ ID NO 4
LENGTH: 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
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RESULT 11

US-08-474-140-11

Sequence 11. Application US/08474140

Patent No. 5721127

GENERAL INFORMATION:

PAPLICANT: DEMERER, PHILIPPE

APPLICANT: DEMERER, PHILIPPE

APPLICANT: DEMERER, PHILIPPE

TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH

TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF

TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF

TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF

TOTHER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS: 15

CONPUTER: OS SECRET, N.W., SUITE 200

STATE: D.C.

STATE: D.C.

COMPUTER: ELOPDY disk

COMPUTER: IBM PC COMPATIBLE

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

SOFTWARE: PAPLICATION DATE: 05-014-1995

CLASSIFICATION NUMBER: 4121-41

TELECOMMUNICATION INFORMATION:

REGISERRATION NUMBER: 37,136

TELECOMMUNICATION INFORMATION:

REFERENCE/DOCKET NUMBER: 4121-41

TELECOMMUNICATION INFORMATION:

REFERENCE/DOCKET NUMBER: 37,136

TELECOMMUNICATION INFORMATION:

REFERENCE/DOCKET NUMBER: 4121-41

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
US-08-477-630-11
US-08-477-630.11
Sequence 11, Application US/08477630
Fatent No. 5721128
GENERAL INFORMATION:
APPLICANT: ADMORY, ANYOINE
TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
TITLE OF SEQUENCES: 15
CORRESPONDENCE 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, P.C.
                                                          Gaps
                                                      5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2,
                                                  Indels
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Pred. No. 54;
2; Mismatches 3; Indels
                                              Mismatches
                                          2;
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amino acids
                                 8; Conservative
                                                                                                                                                   628 NPGIALYG--EPWTG 640
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Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                    1 NPTVALYGLKQDWNG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NPTVALYGLKQDWNG 15
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641 NPGIALYG--EPWTG 653
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MOLECULE TYPE: protein
US-08-474-140-11
                                 Matches
                                                                                                                                                           Dp
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                                                                                                                                                                                                                                                                GENERAL INCORDATION:
APPLICANT: Barbet, Anthony F.
APPLICANT: Barbet, Anthony F.
APPLICANT: Barbet, Anthony F.
APPLICANT: Barridge, Michael J.
APPLICANT: Burridge, Michael J.
APPLICANT: Burridge, Michael J.
APPLICANT: Natangirua, Fred R.
APPLICANT: Natangirua, Fred R.
APPLICANT: Mahan, Suman M.
ITILE OF INVENTION: Animals and Humans
FILE REFERENCE: UF-167C1
CURRENT APPLICATION NUMBER: US/08/953,326
CURRENT FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/953,326
SARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-17
SOFTWARE: PETING DATE: 1996-10-17
SOFTWARE: PETING DATE: 1996-10-17
SOFTWARE: PETING DATE: 1996-10-17
SOFTWARE: PETING DATE: 133
MUNDER OF SEO ID NOS: 24
LENGTH: 133
MUNDER OF SEO ID NOS: 24
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Pred. No. 1.1;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
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Sequence 2, Application US/09346237A
Patent No. 6265197
GENERAL INFORMATION:
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Sevendsen, Allan
TITLE OF INVENTION: Starch Debranching Enzymes
TITLE OF INVENTION NUMBER: US/09/346,237A
CURRENT APPLICATION NUMBER: US/09/346,237A
CURRENT FILING DATE: 1999-07-05
EARLIER FILING DATE: 1999-07-05
EARLIER FILING DATE: 1999-07-05
EARLIER PILING DATE: 1999-07-05
EARLIER FILING DATE: 1999-07-08
EARLIER FILING DATE: 1999-07-08
EARLIER FILING DATE: 1999-07-28
SOSTWARE: FastSEQ for Windows Version 3.0
EDROTH: 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.9%; Score 42; DB 4; 53.3%; Pred. No. 53;
                                                                                                                                                           US-08-953-326-20
; Sequence 20, Application US/08953326
; Patent No. 6251872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Bacillus deramificans FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: PEPTIDE
... LOCATION: (1)...(915)
... CTHER INDERMATION: Pullulanase
US-09-346-237-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Ehrlichia canis
US-08-953-326-20
60 NTTVGVFGIEQDWD 73
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Best Local Similarity
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APPLICANT: DEWEER, PHILIPPE
APPLICANT: MADRY ANTOINE
TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PULLULANASE, PROCESSES FOR THE PREPARATION OF THIS
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
CORRESPONDENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                              Score 42; DB 1; Length 928;
Pred. No. 54;
2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, P.C. STREET: 2000 K Street, N.W., Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-EOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.9%; Score 42; DB 53.3%; Pred. No. 54; iive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/474,545 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Wilhiem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-43
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-1850
TELEFAX: 650 383-5605
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/08474545
Patent No. 5736375
GENERAL INFORMATION:
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 928 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                   42.98;
53.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 928 amino acids
amino acids
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Best Local Similarity 53.3
Matches 8; Conservative
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641 NPGIALYG--EPWTG 653
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641 NPGIALYG--EPWTG 653
                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-472-293-11
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                                                                                                                                                                                                                                                                                                                                     1 NPTVALYGLKQDWNG 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington STATE: D.C.
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Matches 8; Conserv
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US-08-474-545-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-474-545-11
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Patent No. 5731174
GENERAL INFORMATION:
APPLICANT: DEMER, PHILIPPE
APPLICANT: AMORY; ANTOINE
TITLE OF INVENTION: PULLUILANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PULLUILANASE AND THE USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5;
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Pred. No. 54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: WILLIAN BRINKS HOFFR GILSON & LIONE, P.C. 2000 K Street, N.W., Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,293
FILING DATE: 07-JUN-1995
                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,630
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
      2000 K Street, N.W., Suite 200
                                                                                                                                                                                                                                                                                                       ATCRNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-42
TELEPHONE: (202) 299-1850
TELEPHONE: (202) 299-1850
TELERAX: (202) 299-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 928 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Wilhlem F. Gadiano, Esq. REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-44
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 53.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-477-630-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NPTVALYGLKQDWNG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington
                             Washington
                                                                      U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-08-472-293-11
                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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RESULT 15

Sequence 11, Application US/08478341

Sequence 11, Application US/08478341

Sequence 11, Application US/08478341

Sequence 11, Application US/08478341

Patent No. 5817498

APPLICANT: DEBEER: PHILIPPE

TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH

TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF

TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF

TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF

CORRESPONDENCE ADDRESSS:

ADDRESSEE: WILLIAM BRINGS HORE GILSON & LIONE, P.C.

CITY: Washington

CITY: Washington

COUNTRY: U.S.A.

STATE: 2000 K Street, N.W., Suite 200

CONPUTER: READABLE FORM:

MEDIUM TYPE: PATENTION OF PC-DOS/MS-DOS

SOFTWARE: OF-DOS/MS-DOS

CORPATION SYSTEM: PC-DOS/MS-DOS

SOFTWARE: OF-DOS/MS-DOS

CORPATION SYSTEM: PATENTION:

MAME: WILLIAM PR. Gadiano, ESG

TELLOR DATA: 1056

ATTORNEY/AGRITINO NUMBER: US/OS/M78, 341

FILLING DATE: TO DATA: 136

REFERENCE/DOCKET NUMBER: 37, 136

TELEPHONE: (202) 291-1850

TELEPHONE: TELEPHONE: (202) 291-1850

TELEPHONE: (202) 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Query Match

42.9%; Score 42; DB 2; Length 928;
Best Local Similarity 53.3%; Pred. No. 54;

Matches 8; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NPTVALYGLKQDWNG 15
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Search completed: March 14, 2002, 09:07:40 Job time: 841 sec

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E. chafeensis OMP-E. chafeensis p28 Ehrlichia chaffeen Ehrlichia chaffeen Variable surface a

Ehrlichia chaffeen Bhrlichia chaffeen Major antigenic pr E. chafeensis OMP-Ehrlichia canis im

E. canis P30-1 pro
Cowdria ruminatium
Cowdria ruminatium
Cowdria ruminatium
Major antigenic pr
Ehrlichia chaffeen
E. chafeensis OMPEhrlichia chaffeen
Variable surface a
E. canis P30-4 pro
Variable surface a
Ehrlichia canis vs
Ehrlichia canis pa
Ehrlichia canis im

rotal number of

Searched:

Minimum DB s Maximum DB s

Database

Perfect score:

Title:

Sequence:

OM protein

Run on:

Scoring table:

C883P predicted am Bacillus deramific Bacillus deramific Bacillus deramific

pneu

Streptococcus

Pinus Pinus

radiata tran

Pinus radiata tran radiata tran Gene 41 human secr

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Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel outer membrane proteins from Ehrlichia chaffeensis and
                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                       AAY0477
AAY06961
AAW51088
AAB36182
AAU04192
AAW51092
                                                                                                                                                AAY06946
AAB36186
AAU04196
AAU04201
AAW51097
AAW51097
AAX714780
AAY21976
                                                                                                                                                                                                                                                            AAB33357
AAB33358
AAY81775
                                                                                                                                                                                                                                                                                       AAB33257
AAM24509
AAE05695
                                                         AAB36183
AAU04193
                                                                                                                                                                                                                                         AAY21976
AAB44680
                             AAB36189
AAU04199
          AAY06942
                                                 AAW51089
                                                                              AAY06943
                    AAW51095
                                                                                                                                                                                                                                                                                                                   AAE05694
                                                                                                                                                                                                                                                                                                                                                                                                              AAY06945 standard; Protein; 280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 13; Fig 5B; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E. chafeensis OMP-1C protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-US19600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0059353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (OHIS ) UNIV OHIO STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohashi N, Rikihisa Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ehrlichia chafeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-254290/21.
N-PSDB; AAX34745.
Ehrlichia canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    detection; dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9913720-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-1999.
 AAY06945;
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 RESULT
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E. canis P30-2 pro
Ehrlichia canis im
Ehrlichia chaffeen
Ehrlichia chaffeen
Variable surface a
E. canis P30 prote
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Ehrlichia chaffeen
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Ehrlichia chaffeen
                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                /SIDSB/goddata/geneseq/geneseqp/AA1990.DAT:*
/SIDSB/goddata/geneseq/geneseqp/AA1991.DAT:*
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                 hits satisfying chosen parameters:
                                                                                                                                                                              522463 seqs, 74073290 residues
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Maximum Match 100%
Listing first 45 summaries
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AAU04197
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AAY71479
AAW51094
AAB36188
AAU04198
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                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                            1 NPTVALYGLKQDWNGVSA 18
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        The invention provides isolated outer membrane proteins (OMP) from Brilithia chafeensis and E. canis. The E. Chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in AAX'06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAX'06599-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Composition containing nucleic acid encoding rickettsial antigenuseful for, e.g. stimulating protective immune response in humans or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is the full-length variable surface antigen VSA3 protein of Ehrlichia chaffeensis. Its amino acid sequence was deduced from a partial open reading frame (ORF5) of a genomic locus (see AAV07179) of E. chaffeensis that was obtained on the basis of homology to the major antigenic protein MAPI (see AAW1088) of Cowdria ruminantium. This genomic locus included 5 ORFS encoding similar, but non-identical proteins (see AAW51081-95). A claimed composition comprises a nucleic acid (see AAW51075-82) encoding a polypeptide (see AAW51089-99) that elicits a protective immune response against rickettsial pathogen. The nucleic acid is used, in human or veterinary medicine, in vaccines to protect against Rickettsia, Ehrlichia, Anaplasma and Cowdria species. The Ehrlichia antigenic
                                                                                                                                                   .;
0
                                                                                                                            Length 280;
                                                                                                                                                                                                                                                                                                                                               MAP1 homologue; variable surface antigen; VSA3; rickettsia; DNA vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McGuire TC;
                                                                                                                                                  Indels
                                                                                                                           Score 98; DB 20;
Pred. No. 6.7e-09;
Mismatches 0;
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/note= "putative signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ganta RR,
                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                         AA.
                                                                                                                                                                                                                                                                                                                          Ehrlichia chaffeensis VSA3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Fig 2A-B; 39pp; English.
                                                                                                                                                                                                                                                       278
                                                                                                                         Query Match

Best Local Similarity 100.0%; P

Matches 18; Conservative 0;
                                                                                                                                                                                                                                                      AAW51093 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-US19044
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                                                                                                                                                                       1 NPTVALYGLKQDWNGVSA 18
                                                                                                                                                                                     Barbet AF, Burridge MJ,
Nyika A, Rurangirwa FR;
                                                                                                                                                                                                                                                                                                                                                                                   Ehrlichia chaffeensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYFL ) UNIV FLORIDA.
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                                                                                          280 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-APR-1998
                                                                                          Sequence
                                                                                                                                                                                                                                                                             AAW51093;
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                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30;
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0
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polypeptides can be used diagnostically to detect antibodies associated with Ehrlichia infection (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 278;
                                                                                                             Length 278;
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Pred. No. 3.6e-07;
2; Mismatches 1; Indels
                                                                                                                                               Indels
                                                                                              DB 19; Le. 3.6e-07;
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Pred. No. 3.6e
2; Mismatches
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                                                                                                                                                                                                                                                                                                                AAY06947 standard; Protein; 278
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                                                                                                                                                                                                                                                                                                                                                                                                                           E. chafeensis OMP-1E protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0059353.
                                                                                                         Query Match 89.8%;
Best Local Similarity 83.3%;
Matches 15; Conservative
                                                                                                                                                                                    1 NPTVALYGLKQDWNGVSA 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ehrlichia chafeensis.
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection; dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-SEP-1997;
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AAY06947
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AAB36187
ID AAB3
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antigen 3 (VSA3) isolated from Ehrlichia chaffeensis, which has similarity to major antigen protein (MAP). The MAP polynucleotides and polypeptides are useful as vaccines for conferring immunity to rickettsia infection, including Cowdria ruminantium causing heartwater. The MAP polynucleotides may be used as molecular markers in nucleic acid analysis procedures, and to produce the MAP polypeptides, which may be used to raise antibodies that are reactive with the polypeptides. The nucleic acids may further be used as probes to identify complementary sequences within other nucleic acid molecules or genomes, where such probes can be applied to identify or distinguish infectious strains of organisms in diagnostic procedures or in rickettaial research where identification of particular organisms or strains is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence represents the amino acid sequence of variable surface
                                                                                                                                                                                                                                                                                                                                                                                                       New MAP2 genes and polypeptides useful as vaccines for conferring immunity to human and animal rickettsial diseases, e.g. heartwater as molecular markers in nucleic acid analysis procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30; detection; dog.
                                                                                                                                                                                                                                                                             Barbet AF, Ganta RR, McGuire TC, Burridge MJ, Rurangirwa FR, Mahan SM, Bowie MV, Alleman AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Fig 2A-2B; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY06962 standard; Protein; 280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.8%;
                                                                                                                                                 97US-0953326.
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Best Local Similarity 83.3
Matches 15; Conservative
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                        Ehrlichia chaffeensis.
                                                                                                                                                                                                                                      (UYFL ) UNIV FLORIDA.
                                                                                                                                                                                                                                                                                                                                           WPI; 2001-424487/45.
N-PSDB; AAS07578.
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                                                                  US6251872-B1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antigenic protein 1 (MPP) of Ehrlichia sp. The MAPI gene may be used in a vaccines to protect animals or humans against rickettsial diseases caused by a organisms of Rickettsia sp., Ehrlichia sp., Anaplasma sp. or Cowdria sp. The vaccine elicits an immune response protective against the rickettsial pathogen. The nucleic acid vaccines can be driven by the human cytomegalvoirus (HCW) enhancer-promoter. Cowdria ruminatium genes designated map 2, Ihworf3, 4hworf1, 18hworf1 and 3gdorf3 may be used in therapeutic and diagnostic applications. The polypeptides are useful for detecting antibodies associated with infection by a rickettsial pathogen whilst the polynucleotides may be used to detect the presence of rickettsial nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides useful as DNA vaccines for conferring immunity to rickettsial infection e.g. heartwater caused by Cowdria ruminantium, comprises major antigenic protein 1 or 2 gene of rickettsial pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McGuire TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence shows a high degree of similarity to the major
                                                                                                                         Ehrlichia chaffeensis, VSA3; variable surface antigen 3; MAP1; major antigenic protein 1; antirickettsial; vaccine; gene therapy; Rickettsia; Cowdria; Anaplasma; map2; lhworf3; 4hworf1; 18hworf1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Major antigenic protein 1; MAP1; vaccine; immunogenic; rickettsia; infection; heartwater; diagnostic; variable surface antigen; VSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ganta RR, Burridge MJ, Mahan SM, McGuire
nd AL, Simbi BH, Whitmire WW, Alleman AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 88; DB 21; Length 278;
Pred. No. 3.6e-07;
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                                                                                    Ehrlichia chaffeensis partial VSA3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 44-45; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barbet AF, Bowie MV, Ganta Rurangirwa FR, Moreland AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89.8%;
                                                                                                                                                                                                                                                                                                                                                               21-APR-2000; 2000WO-US10886
                                                                                                                                                                                                                                                                                                                                                                                                       99US-0130725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NPTVALYGLKQDWNGVSA 18
                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15; Conservative
                                                                                                                                                                                                                                      Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYFL ) UNIV FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-679675/66.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                278 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAC68704.
                                                                                                                                                                                                                                                                           WO200065063-A2
                                                                                                                                                                                                                                                                                                                                                                                                         22-APR-1999;
                                          02-MAR-2001
                                                                                                                                                                                                                                                                                                                     02-NOV-2000
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AAB36187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU04197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                            3gdorf3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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NAMES OF COLOR OF STREET STREE

RESULT ΩX

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Gaps

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Indels

Length 278;

Score 88; DB 22; Len;

heartwater, or

Nyika A;

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ehrlichiosis in dogs
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                                                                                                                                                                                                                                                              RESULT
AAW51094
                                                                                                                                                                                                                                                                                       Пр
δà
                                                                                                                                                                                                                            ó;
                                                                                                                    The invention provides isolated outer membrane proteins (OMP) from brillonia chafeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in AAY06943-958 The E. canis proteins form part of the P30 family and consist of proteins shown in AAY06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                                                                                                                                                                                                                                         Homologous 28-kDa protein gene; ECa28SA3; immunoreactive; vaccine; p28 gene; polymorphic multiple gene family; immunoprotective antigen; antibacterial; canine ehrlichiosis; canine tropical pancytopaenia; tick-borne rickettaial disease; serodiagnosis.
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ehrlichia canis antigens useful for vaccinating against canine
                                                                                                                                                                                                                            0;
                                                                                                                                                                                                         Score 62; DB 20; Length 280;
Pred. No. 0.011;
2; Mismatches 3; Indels
                                                                             Novel outer membrane proteins from Ehrlichia chaffeensis Ehrlichia canis
                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
11.23
7.label- Signal_peptide
24.280
7label= Mature_ECa28SA3_28-kDa_protein
                                                                                                                                                                                                                                                                                                                                                            Ehrlichia canis immunoreactive protein ECa28SA3.
                                                                                                        Disclosure; Fig 22B; 55pp; English.
                                                                                                                                                                                                                                                                                                         AAY71479 standard; Protein; 280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Walker DH, Yu X, McBride JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0201458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-412298/35.
N-PSDB; AAD01294, AAD01295.
  97US-0059353.
                                                                                                                                                                                                            Query Match 63.3%;
Best Local Similarity 66.7%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                           12-OCT-2000 (first entry)
                                                                                                                                                                                                                                              1 NPTVALYGLKQDWNG 15
                                                                                                                                                                                                                                                          | || ::||| ||||
| nstvgvfglkhdwng 73
                  (OHIS ) UNIV OHIO STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (RERE-) RES DEV FOUND.
                                   Ohashi N, Rikihisa Y;
                                                   WPI; 1999-254290/21.
N-PSDB; AAX34762.
                                                                                                                                                                                   280 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                       Ehrlichia canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200032745-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-NOV-1998;
03-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-NOV-1999;
 19-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-JUN-2000
                                                                                                                                                                                                                                                                                                                           AAY71479;
                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                59
                                                                                                                                                                                                                                                                                          RESULT
AAY71479
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The patent relates to homologous 28-KiloDalton (KDa) protein genes of Ehrlichia canis, designated ECa28SA1, ECa28SA3, ENCA28-1 and and contained in a single locus of 5.592 kb. The 28-KDa proteins are immunoreactive with anti-E. can's serum hence are important against E. can's infections such as canine ehrlichiosis in dogs. Canine ehrlichiosis, also known as canine tropical parcytopeania, is a tick-borne rickettsial disease of dogs. ECa28-1 is conserved amongst different strains of E. canis and hence useful for serodiagnosis of canine ehrlichiosis. The present sequence is a E. canis ECA28SA3 30-KDa protein which is post-translationally modified to a mature 28-KDa protein by cleavage of N-terminal signal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Composition containing nucleic acid encoding rickettsial antigen - useful for, e.g. stimulating protective immune response in humans or animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is the full-length variable surface antigen VSA4 protein of Ehrlichia chaffeensis. Its amino acid sequence was deduced from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 62; DB 21; Tength 280;
Pred. No. 0.011;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAP1 homologue; variable surface antigen; VSA4; rickettsia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McGuire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "putative signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mahan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1..25
Claim 12; Page 68-69; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ehrlichia chaffeensis VSA4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ganta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW51094 standard; Protein; 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Fig 2B; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.3%;
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Nyika A, Rurangirwa FR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NPTVALYGLKQDWNG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | || ::||| ||||
59 nstvgvfglkhdwng 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYFL ) UNIV FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-251232/22.
N-PSDB; AAV07179.
                                                                                                                                                                                                                                                                                                                                                                                                                                   280 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9816554-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-APR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW51094;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides useful as DNA vaccines for conferring immunity to rickettsial infection e.g. heartwater caused by Cowdria ruminantium, comprises major antigenic protein 1 or 2 gene of rickettsial pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McGuire TC;
partial open reading frame (ORF4) of a genomic locus (see AAV07179) of E. chaffeensis that was obtained on the basis of homology to the major antigenic protein MAPI (see AAW1088) of Cowdria ruminantium. This genomic locus included 5 ORFs encoding similar, but non-identical proteins (see AAW51091-95). A claimed composition comprises a nucleic acid (see AAW51075-82) encoding a polypeptide (see AAW51088-99) that elicits a protective immune response against rickettsial pathogen. The nucleic acid is used, in human or veterinary medicine, in vaccines to protect against Rickettsia, Ehrlichia, Anaplasma and Cowdria species. The Ehrlichia antigenic associated with Ehrlichia infection (claimed).
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             major antigenic protein 1; antirickettsial; vaccinė; gene therapy; Rickettsia; Cowdria; Anaplasma; map2; lhworf3; 4hworf1; 18hworf1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mahan SM, McGuire
re WW, Alleman AR;
                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ehrlichia chaffeensis; VSA4; variable surface antigen 4; MAP1;
                                                                                                                                                                                                                                                                                               Score 61; DB 19; Length 280; Pred. No. 0.017;
                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Burridge MJ, Mahan
oi BH, Whitmire WW,
                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barbet AF, Bowie MV, Ganta RR, Burrid
Rurangirwa FR, Moreland AL, Simbi BH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ehrlichia chaffeensis partial VSA4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 45-46; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB36188 standard; Protein; 280 AA.
                                                                                                                                                                                                                                                                                               62.2%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-APR-2000; 2000WO-US10886
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                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                        | |: ::||||||:|
nttigvfglkqdwdg 74
                                                                                                                                                                                                                                                                                                                                                                   1 NPTVALYGLKQDWNG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ehrlichia chaffeensis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-679675/66.
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                           280 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB36188;
                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                                       09
                                                                                                                                                                                                                                                                                                                                 Matches
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and 3gdorf3 may be used in therapeutic and diagnostic applications. The polypeptides are useful for detecting antibodies associated with infection by a rickettsial pathogen whilst the polynucleotides may be used to detect the presence of rickettsial nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New MAP2 genes and polypeptides useful as vaccines for conferring immunity to human and animal rickettsial diseases, e.g. heartwater, or as molecular markers in nucleic acid analysis procedures
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence represents the amino acid sequence of variable surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Major antigenic protein; MAP; vaccine; immunogenic; rickettsia; infection; heartwater; diagnostic; variable surface antigen; VSA.
                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                      Variable surface antigen 4 (VSA4) from Ehrlichia chaffeensis.
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                                                                                                                                        Score 61; DB 21; Length 280;
Pred. No. 0.017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nyika A;
                                                                                                                                                                          Indels
                                                                                                                                                                         5;
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, Alleman AR;
                                                                                                                                                        Pred. No. 0.014; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SM, Bowie MV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Fig 2A-2B; 30pp; English.
                                                                                                                                                                                                                                                                                                                                  AAU04198 standard; Protein; 280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McGuire TC,
                                                                                                                                        62.2%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0953326.
                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                | |: ::|||||:|
60 nttigvfglkgdwdg 74
                                                                                                                                                                                                           1 NPTVALYGLKQDWNG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rurangirwa FR, Mahan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ganta RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYFL ) UNIV FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-424487/45.
                                                                                                                                        Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                        280 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAS07578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6251872-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-0CT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                      23-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUN-2001.
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                                                                                                                                                                                                                                                                                                                                                                    AAU04198;
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                                                                                         Sequence
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RESULT

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The invention provides isolated outer membrane proteins (OMP) from behilding chafeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in AAY06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAY06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30; detection; dog.
                                                                                                                                                                                                                                                                   Novel outer membrane proteins from Ehrlichia chaffeensis and
Ehrlichia canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 58; DB 20; Length 280;
Pred. No. 0.057;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
AAY06942
ID AAX06942 standard; Protein; 256 AA.
                                                                                                                                                                                                                                                                                                               Claim 16; Fig 8B; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-0059353.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.2%;
60.0%;
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                                                                                                               98WO-US19600.
                                                                                                                                           97US-0059353.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E. chafeensis p28 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 59.3
Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (OHIS ) UNIV OHIO STATE.
                                                                                                                                                                    (OHIS ) UNIV OHIO STATE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74
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                                                                                                                                                                                                   Ohashi N, Rikihisa Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 ntttgvfglkgdwdg
                            Ehrlichia chafeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ehrlichia chafeensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-254290/21.
N-PSDB; AAX34742.
                                                                                                                                                                                                                              WPI; 1999-254290/21.
N-PSDB; AAX34748.
                                                                                                                                                                                                                                                                                                                                                                                                                                                280 AA;
detection; dog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9913720-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-SEP-1997;
                                                      WO9913720-A1.
                                                                                                               18-SEP-1998;
                                                                                                                                         19-SEP-1997;
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                                                                                  25-MAR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY06942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30;
                                                                                                                                                                                                                                                        Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30; detection; dog.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel outer membrane proteins from Ehrlichia chaffeensis Ehrlichia canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
               Indels
               2;
Pred. No. 0.017;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d. No. 0.03
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 59;
Pred. No. 0
4; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY06948 standard; Protein; 280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 19B; 55pp; English.
                                                                                                                                             288 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E. chafeensis OMP-1F protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 60.2%;
Best Local Similarity 52.9%;
Matches 9; Conservative
                                                                                                                                             AAY06959 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0059353
60.08;
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                                                                                                                                                                                                       (first entry)
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60 ntttgvfglkgdwdgat 76
Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              (OHIS ) UNIV OHIO STATE.
                                          1 NPTVALYGLKODWNG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohashi N, Rikihisa Y;
                                                           | |: ::|||||:|
60 nttigvfglkgdwdg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-254290/21.
N-PSDB; AAX34759.
                                                                                                                                                                                                                                E. canis P30 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288 AA;
                                                                                                                                                                                                                                                                                                      Ehrlichia canis.
                                                                                                                                                                                                                                                                                                                                  WO9913720-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                     19-SEP-1997;
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                                                                                                                                                                                                     05-JUL-1999
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Gaps

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Gaps

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The present sequence shows a high degree of similarity to the major antigenic protein 1 (MAP1) of Ehrlichia sp. The MAP1 gene may be used in a vaccines to protect animals or humans against rickettsial diseases caused by a organisms of Rickettsia sp., Ehrlichia sp., Anaplasma sp. or Cowdria sp. The vaccine elicits an immune response protective against the rickettsial pathogen. The nucleic acid vaccines can be driven by the human cytomegalovirus (HCMV) enhancer-promoter. Cowdria ruminatium genes designated map 2, 1hworf3, 4hworf1, 18hworf1 and 3gdorf3 may be used in therapeutic and diagnostic applications. The polypeptides are useful for detecting antibodies associated with infection by a rickettsial pathogen whilst the polynucleotides may be used to detect the presence of rickettsial nucleic acids.
nucleic acid (see AAV07176-82) encoding a polypeptide (see AAW51088-99) that elicits a protective immune response against a rickettsial pathogen. The nucleic acid is used, in human or veterinary medicine, in vaccines to protect against Rickettsia, Ehrlichia, Anaplasma and Cowdria species. The Ehrlichia antigenic polypeptides can be used diagnostically to detect antibodies associated with Ehrlichia infection (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides useful as DNA vaccines for conferring immunity to rickettsial infection e.g. heartwater caused by Cowdria ruminantium, comprises major antigenic protein 1 or 2 gene of rickettsial pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mahan SM, McGuire TC;
re WW, Alleman AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ehrlichia chaffeensis; VSA5; variable surface antigen 5; MAP1; major antigenic protein 1; antirickettsial; vaccine; gene therapy; Rickettsia; Cowdria; Anaplasma; map2; lhworf3; 4hworf1; 18hworf1;
                                                                                                                                                                                                                            ;
                                                                                                                                                                                         Score 57; DB 19; Length 276; Pred. No. 0.083;
                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ganta RR, Burridge MJ, Mahan 9
nd AL, Simbi BH, Whitmire WW,
                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ehrlichia chaffeensis partial VSA5.
                                                                                                                                                                                                                                                                                                                                                                                  AAB36189 standard; Protein; 276 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 47; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rurangirwa FR, Moreland AL,
                                                                                                                                                                                          58.2%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-APR-2000; 2000WO-US10886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0130725
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                          1 NPTVALYGLKQDWNG 15
                                                                                                                                                                                                                                                                                | || ::||||:|
59 nttvgvfglkqnwdg 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ehrlichia chaffeensis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYFL ) UNIV FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-679675/66.
                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                         276 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                   AAB36189;
                                                                                                                                          Sequence
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                                                                                The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in AAY06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAY06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Composition containing nucleic acid encoding rickettsial antigen - useful for, e.g. stimulating protective immune response in humans or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the near full-length variable surface antigen VSA5 protein of Ehrlichia chaffeensis; it lacks about 5-7 C-terminal amino acid residues. The VSA5 amino acid sequence was deduced from a partial open reading frame (ORFS) of a genomic locus (see AAN07179) of E. chaffeensis that was obtained on the basis of homology to the major antigenic protein MAPI (see AAW51089) of Cowdria ruminantium. This genomic locus included 5 ORFs encoding similar, but non-identical proteins (see AAW51091-95). A claimed composition comprises a
                                                                                                                                                                                                                                                                                            ;
 Novel outer membrane proteins from Ehrlichia chaffeensis and
                                                                                                                                                                                                                                                            Score 57; DB 20; Length 256; Pred. No. 0.076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAP1 homologue; variable surface antigen; VSA5; rickettsia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ganta RR, Mahan SM, McGuire TC;
                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ehrlichia chaffeensis VSA5 protein (partial sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "putative signal peptide"
                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW51095 standard; Protein; 276 AA
                                                   Claim 18; Fig 1; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Fig 2B; 39pp; English.
                                                                                                                                                                                                                                                          58.2%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-US19044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                              48
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| 34 nttvgvfglkgnwdg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-251232/22.
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                         256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAV07179
                     Ehrlichia canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9816554-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-0CT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA vaccine
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                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW51095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
   δλ
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SQ Sequence 276 AA;
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0; Ouery Match 58.2%; Score 57; DB 21; Length 276; Best Local Similarity 60.0%; Pred. No. 0.083; Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 1 NPTVALYGLKQDWNG 15 | | | ::||||:|| 59 nttvgvfglkqnwdg 73 pp δy

Search completed: March 14, 2002, 09:09:37 Job time: 428 sec

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Q9s6h1 cowdria rum
Q9s6h0 cowdria rum
Q9xd58 pseudomonas
Q9sis4 arabidopsis
 ehrlichia c
ehrlichia c
ehrlichia c
ehrlichia c
deinococcus
                                                                                                                                                        COWGTIA TUM
                                                                                                                     salmonella
pasteurella
cowdria rum
                                                                                                                                                                                                                                                                008721 rattus norv
046328 cowdria rum
                                                                cowdria sp.
                                                                                            cowdria rum
cowdria rum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of Ehrlichia chaffeensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular characterization of a 28 kDa surface antigen gene family of the tribe Ehrlichiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE-EROM N.A.
STRAIN=ARRANSAS;
MEDLINE-98321180; PubMed-9647746;
Reddy G.R., Sulsona C.R., Barbet A.F., Mahan S.M., Burridge M.J.,
Alleman A.R.;
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 09zgjl e
09f475 e
052106 e
052104 e
09rwl0 d
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0915f8
095k3 f
09af98
09af98
046329
046331
046332
046332
046333
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Q46327
Q9afa1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OMP-1D.
Ehrlichia chaffeensis.
Ehrlichia proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Ehrlichieae; Ehrlichieae; NCBI_TaxID=945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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EMBL; U72291; AAC02338.1; -.

EMBL; AF062761; AAC26718.1; -.

InterPro; IPRO02566; Surface_Ag_msp4.

Pfam; PF01617; Surface_Ag_2.2; 1.

SEQUENCE 286 AA; 31509 MW; F145A79270F386BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 105; DB 2;
Best Local Similarity 100.0%; Pred. No. 3.1e-09;
Matches 19; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98084465; FubMed=9423849;
Ohāshi N., Zhi N., Zhang Y., Rikhhisa Y., Immunodominant major outer membrane proteins in ercoded by a polymorphic multigene family. Infect. Immun. 66:132-139(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                         286 AA
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                                                                                                                                                                                                                                                                008721
                                                                                                                                                                                                                                                                                          0986H1
0986H0
09XD58
09XIS4
                                                                                                                                Q9CKK3
Q9AF99
Q9AF98
Q46331
Q9R425
Q46334
Q46332
Q46332
            Q9F475
O52106
O52104
Q9RW10
                                                               09AMF6
046327
09AFA1
09AEU3
09L5F8
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06,
17,
                                                    1 NTTVGVFGIEQDWDRCVIS 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
01-JUN-1998
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1998
052105
052105;
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095412 ehrlichia c
097415 ehrlichia c
095817 ehrlichia c
085816 ehrlichia c
085816 ehrlichia c
085818 ehrlichia c
095493 ehrlichia c
097689 ehrlichia c
097688 ehrlichia c
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                                                                                         Search time 103.37 Seconds
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Q9r8a5 e
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                       473505 seqs, 146272329 residues
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                                                                                         March 14, 2002, 09:24:09;
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Maximum Match 100%
Listing first 45 summaries
                                                               - protein search, using sw model
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1 NTTVGVFGIEQDWDRCVIS
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1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_inwan:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*
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sp_vertebrate:*
sp_unclassified:*
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MEDLINE-980844465, PubMed-9423849;
Ohashi N., Zhi N., Zhang Y., Rikihisa Y.;
"Immunodominant major outer membrane proteins of Ehrlichia chaffeensis are encoded by a polymorphic multigene family.";
Infect. Immun. 66:132-139(998).
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MEDLINE-21153566; PubMed-11254561;
MEDLINE-21153566; PubMed-11254561;
Manalysis of Transcriptionally Active Gene Clusters of Major Outer
Menalysis of Transcriptionally Active Gene Clusters of Major Outer
Menalysis of Transcriptionally in Ehrlichia canis and E.
Menaffeensis., 69:2083-2091(2001).
Infect. Immun 69:2083-2091(2001).
EMBL; 072291; AAK28673.1; -.
SEQUENCE 281 AA; 30343 MW; A99E5F7C4459AA9A CRC64;
                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-UNOV-2001 (TrEMBLrel. 08, Last sequence update)
28 KDA MAJOR SURFACE ANTIGEN-5 (FRACMENT).
28 KDA MAJOR SUFFACE ANTIGEN-5 (FRACMENT).
BACTEATIA: Protecobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
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sacteria, Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Ehrlichieae; Ehrlichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 73; DB 2; Length 276 Pred. No. 0.0005; 3; Mismatches 3; Indels
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN P28.
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Best Local Similarity 68.4%;
Matches 13; Conservative 3
60 NTTTGVFGLKQDWDGSTIS 78
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SEQUENCE FROM N.A.
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085358;
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SEQUENCE FROM N.A.

STRAIN-ARKANSAS;

WEDLINE-98084465; PubMed-9423849;

Chashi N., Zhi N., Zhang Y., Rikihisa Y.;

Immunodomlanat major outer membrane proteins of Ehrlichia chaffeensis are encoded by a polymorphic multigene family.";

EMBL; U72291; AAC02940.1;

EMBL; U72391; AAC03940.1;

EMBL; U72391; AAC03940.1;

EMBL; U72391; U7331 MW; CCAA6C34E2AF393E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular characterization of a 28 kDa surface antigen gene family of the tribe Bhrischiae.";
Biochem. Biophys. Res. Commun. 247:636-643(1998).
EMBL; AF062761; AAC26720.1; .
InterPro: IPR002566; Surface_Ag_msp4.
Penis, PF01617; Surface_Ag_ms, 1.
SEQUENCE 280 AA; 30743 MW; FBBB41DAF08EE4DC CRC64;
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MEDLINE-98321180; PubMed-9647746;
Reddy G.R., Sulsona C.R., Barbet A.F., Mahan S.M., Burridge M.J.,
Alleman A.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
28 KDA MAJOR SURRACE ANTIGEN-4.
Ehrlichia chaffeensis.
Bacteria, Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae, Ehrlichieae; Ehrlichia.
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Bacteria, Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
NCBL_maxID=945;
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73.3%; Score 77; DB 2; Length 280;
Best Local Similarity 68.4%; Pred. No. 0.00011;
Matches 13; Conservative 3; Mismatches 3; Indels
Matches 13; Conservative 4; Mismatches 3; Indels
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PRELIMINARY;
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STAIN=ST.VINCEMTY.
MEDLINE—99175207; PubMed=10074538;
MEDLINE—99175207; PubMed=10074538;
MEDLINE—99175207; PubMed=10074538;
Thuman isolates of Ehrlichia chaffeensis.";
Thuman isolates of Ehrlichia chaffeensis.";
L. J. Clin. Microbiol. 37:1137-1143(1999).
R InterPro; IPR001702; Gram.—Reg_porin.
R InterPro; IPR001202; Gram.—Reg_porin.
R Pfam; PF01617; Surface_Ag_2; R
R Pfam; PF01617; Surface_Ag_2: T
R PRINTS; PR00182; ECOLNEIPORIN.
The NON_TER T 1 SeQUENCE 246 AA; 26884 MW; C9776392C5129A2F CRC64;
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Rickettsiaceae; Ehrlichieae; Ehrlichia.
NCBL_TaxID=945;
                                         Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 246;
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YU X.-J., Walker D.H.;
"Ehrlichia chaffeensis 28 kDa outer membrane protein.";
"Ehrlichia chaffeensis 28 kDa outer membrane protein.";
"Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL: AFO77734; AAC31547.1;
InterPro; IPR002566; Surface_Ag_msp4.
Pfam; PF01617; Surface_Ag_2; 1.
Pfam; PF01617; Surface_Ag_2; 1.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-UNV-2001 (TrEMBLrel. 17, Last annotation update)
00TER MEMBRANE PROTEIN P28 PRECURSOR.
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Last annotation update)
  OUTER MEMBRANE PROTEIN P28 PRECURSOR (FRAGMENT).
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66.7%; Pred. No. 0.0014;
iive 2; Mismatches 4
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01-NOV-1998 (TrEMBLrel. 08, Last seq
01-UNN-2001 (TrEMBLrel. 17, Last ann
0UTER MEMBRANE PROTEIN P28 PRECURSOR
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Best Local Similarity 66.7
Matches 12; Conservative
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                         Ehrlichia chaffeensis.
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Best Local Similarity
Matches 12; Conserv
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                                                                                        NCBI_TaxID=945;
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"Molecular cloning of the gene for a conserved major immunoreactive
28 kilodalton protein of Ehrlichia canis: a potential serodiagnostic
                                                                   Gaps
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"Cloning and characterization of multigenes encoding the immunodominant 30-kilodalton major outer membrane proteins of Ebrischia canis and application of the recombinant protein for serodiagnosis.";
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"A conserved, transcriptionally active p28 multigene locus of Ehrlichia canis."
Gene 254:245-252(2000).
EMBL. ARC/8553; AAC68667.1; -.
EMBL. ARC/853; AAC68667.1; -.
InterPro: IPR002566; Surface_Ag_msp4.
                                                                                                                                                                                                                                                                                                                                                                                                                      Ehrlichia canis.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
                       Length 281;
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Score 73; DB 2; Length 201. Pred. No. 0.00052;
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SEQUENCE 288 AA; 31590 MW; 86DCAECB88E9BF5E CRC64;
                                                                                                                                                                                                                                                                                                         01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
30-KDA MAJOR OUTER MEMBRANE PROTEIN (P28-8).
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Last annotation update)
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Pred. No. 0.0011;
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                                                              3; Mismatches
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MEDLINE-98371112; Pubmed-9705412;
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66.78;
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O9RH35;
O1-MAY-2000 (TEMBLE-1 13, 0
01-MAY-2000 (TEMBLE-1 13, 0
01-JUN-2001 (TEMBLE-1 17,
                  ch 69.5%;
1 Similarity 68.4%;
13; Conservative
                                                                                                          1 NTTVGVFGIEQDWDRCVIS 19
                                                                                                                                  60 NTTTGVFGLKQDWDGATI 77
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Best Local Similarity
Matches 12; Conserva
                                            Local Similarity
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MEDLINE-99242757; PubMed-10225842; MCBLINE-99242757; PubMed-1025842; MCBLIde J.W. Yu, Xi, Walker D.H.; Molecular cloning of the gene for a conserved major immunoreactive 28.kilodalton protein of Ehrlichia canis: a potential serodiagnostic
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SEQUENCE FROM N.A.
STAIN-CARAHOMA;
MEDLINE=21153566; PubMed=11254561;
Ohashi N., Rikhhisa Y., Unver A.;
Analysis of Transcriptionally Active Gene Clusters of Major Outer
Membrane Protein Multigene Family in Ehrlichia canis and E.
Chaffeensis.";
Infect. Immun. 69:2083-2091(2001).
EMBL; ARON9853; AARX8699.1; -.
SEQUENCE 280 AA; 30803 MW; 27238BEIC7E68A91 CRC64;
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SEQUENCE PROM N.A.
SEQUENCE-98371112; PubMed-9705412;
MEDLINE-98371112; PubMed-9705412;
MCIONING and Characterization of multigenes encoding the immunodominant 30-kilodatton major outer membrane proteins c Ehrlichia canis and application of the recombinant protein serodiagnosis.;
J. Clin. Microbiol. 36:2671-2680(1998).
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MCBLINE-JAKE;

MCBLINE-JAKE;

MCBLINE-JAKE,

MCBAIGG J.W., YU X.J., Walker D.H.;

McDride J.W., Z.S. 2502000);

Gene 254:245-252(2000);

EMBL, ARG3744; AAG14361.1;

ELML, ARG3744; AAG14361.1;

FEMBL, ARG9774; NAG14361.1;

FEMBL, ARG9774; NAG14361.1;

SEQUENCE 280 AA; 30762 MW; BE284A4B94FE3123 CRC64;
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09ADV3
01-JUN-2001 (TEMBLrel. 17, Created)
01-JUN-2001 (TEMBLrel. 17, Last sequence update)
01-JUN-2001 (TEMBLrel. 17, Last annotation update)
01-JUN-2001 (TEMBLREL. 17, Last annotation update)
MAJOR OUTER MEBRANE PROTEIN P30-2.
PROTE PROTEIN P30-2.
PROTECTION OF PROTEIN P30-2.
PRICKettsiaceae; Prilichieae; Bhrlichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match. 59.0%; Score 62; DB 2; Length 280; Best Local Similarity 57.9%; Pred. No. 0.032; Matches 11; Conservative 4; Mismatches 4; Indels
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                                                                                                          antigen.";
Clin. Diagn. Lab. Immunol. 6:392-399(1999).
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SEQUENCE FROM N.A.
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NCBI_TaxID=944;
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Q9R8A7;
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STRAIN-LOUISIANA,
MCBride J.W., Yu X.J., Walker D.H.;
"Molecular cloning of a conserved major immunoreactive 28-kilodalton
Protein gene from a polymorphic multiple gene family of Ehrlichia
canis.";
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MCBride J.W., Yu X.J., Walker D.H.;
"Molecular cloning of a conserved major immunoreactive 28-kilodalton
protein gene from a polymorphic multiple gene family of Ehrlichia
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                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
28 KDA OUTER MEMBRANE PROTEIN (FRAGMENT).
Burlichia canis.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Ehrlichieae; Ehrlichia.
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                                                                                                                                                                                                                                                  Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AF082745; AAC64551.1; -.
InterPro; IPR002566; Surface_Ag_msp4.
Pfam; PF01617; Surface_Ag_2; 1.
NON_TER 278 278
SEQUENCE 278 AA; 30485 MW; 697CB6CA413BBA68 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
28 KDA OUTER MEMBRANE PROFEIN (FRAGMENT).
                                    278 AA
                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                    PRT;
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 69.2
Matches 9; Conservative
                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                          2 TTVGVFGIEQDWD 14
                                                                                                                                                                                                                                                                                                                                                                                                                         :||||||:: |||
61 STVGVFGLKHDWD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 TTVGVFGIEQDWD 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ehrlichia canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9R8A8
Q9R8A8;
                                                Q9R8A9;
                                  Q9R8A9
         13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9R8A8
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1D 0988A7

AC 09R8A7

AC 09R8A7

DY 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DY 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DY 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DY 01-MAY-2000 (TrEMBLrel. 17, Last annotation update)

DY 01-MAY-2000 (TrEMBLrel. 17, Last annotation update)

DY 01-MAY-2000 (TrEMBLrel. 17, Last annotation update)

DY 01-MAY-2000 (TREMBLrel. 17, Last sequence update)

DY 01-MAY-2000 (TREMBLRel. 17, Last sequence update)

CO 01-MAY-2000 (TREMBLRel. 17, Last sequence update)

Richard (TREMBLRel. 17, Last sequence update)

RO NOTEL TAXID-944;

RA NOBL-TAXID-944;

RA SEQUENCE FROM N.A.

DR INTER-PROISEARCH CANG-1891, J. -

DR INTER-PROISEARCH CANG-1891, J. -

DR INTER-PROISEARCH CANG-1891, J. -

DR THE-PROISEARCH CANG-1891, J. -

DR THE-PROISEARCH CANG-189, J. -

RA 278 278 278 278 278 278

QUETY MATCH STATEL 278 278

DR THYGVEGIEQDMD 14

DD 61 STYGVEGIEDDMD 14

DD 61 STYGVEGIEDDMD 14

SEarch Completed: March 14, 2002, 09:24:10
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

March 14, 2002, 09:24:51; Search time 32.82 Seconds Run on:

(without alignments) 21.226 Million cell updates/sec

US-09-765-739A-5

Perfect score:

1 NTTVGVFGIEQDWDRCVIS 19 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		schistoso	O35098 mus musculu	P52707 prunus sero	O50048 prunus sero	Q05808 anthonomus	P01533 anemonia su	P00218 thermoplasm		P42833 saccharomyc	Q62951 rattus norv		Q51881 phormidium					P49654 rattus norv			P25941 streptomyce		067005 aquifex aeo					Q58008 methanococc				_	061735 drosophila
SUMMARIES	ID	POLG_CXB1J	SORC_SCHJA	DPY4_MOUSE	MDL3_PRUSE	MDL2_PRUSE	VIT_ANTGR	TXA1_ANESU	FER_THEAC	FLGE_TREPH	HXTD_YEAST	DPY4_RAT	MA2B_MOUSE	NRTB_PHOLA	MLTB_ECOLI	Y028_ARCFU	YA67_METTH	P2X3_HUMAN	P2X3_RAT	SYFB_AERPE	YLX5_CAEEL	AFSR_STRCO	S190_YEAST	FLGA_AQUAE	SYR_AERPE	BIOB_HELPJ	BIOB_HELPY	DHYS_NEUCR	Y588_METJA	V51K_ACLSP	EX5A_ECOLI	UVRB_TREPA	FHUE_ECOLI	CLOC_DROME
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	Length	2182	171	572	573	576	1790	46	142	463	540	564	1012	279	361	371	377	397	397	548	751	993	1033	223	644	282	282	353	430	460	608	668	729	1023
d	% Query Match	42.4	40.0	39.0	39.0	39.0	38.6	38.1	38.1	38.1	38.1	38.1	38.1	37.1	37.1	37.1	37.1	37.1	37.1	37.1	37.1	37.1	37.1	36.7	36.7	36.2	36.2	36.2	36.2	36.2	36.2	36.2	36.2	36.2
	Score	44	42	41	41	4	40.5	40	40	40	40	40	40	39	39	39	39	33	39	39	39	39		38.5		38	38	38	38	38	38	38	38	38
	Result No.		7	3	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

P34703 caenorhabdi		P22925 petunia hyb	P14317 homo sapien	Q03053 c genome po	P95649 rhodobacter	P54461 bacillus su	P50171 mus musculu	P39767 rhodopseudo	P52348 human herpe	Q58224 methanococc
EMB5_CAEEL	1020_MEDTR	HSD_PETHY	IS1_HUMAN	OLG_CXB5P	BBY_RHOSH	QEU_BACSU	HB8_MOUSE	ORI_RHOBL	rP19_HSV6U	HYS_METJA
		, ,	_	_	, ,	-	_	7	ر ب	-
1521	268	419	486	2185	230	256	260	289	299	351
36.2	35.7	35.7	35.7	35.7	35.2	35.2	35.2	35.2	35.2	35.2
38	37.5	37.5	37.5	37.5	37	37	37	37	37	37
34	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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                                                  01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-AUG-1988 (Rel. 08, Last sequence update)
020-AUG-010 (Rel. 40, Last annotation update)
GENDALPOYDEIN (CONTAINS: COAT PROTEIN VP4 (PIA); COAT PROTEIN VP2 (PIB); COAT PROTEIN VP3 (PIC); COAT PROTEIN VP3 (PIC); COAT PROTEIN P2B; CORE PROTEIN P2C; CORE PROTEIN P2B; GENOME-LINKED PROTEIN VPG (PBB); PICORNAIN 3C (EC 3.4.22.28)
PROTEINSED FROTEIN VPG (PBB); PICORNAIN 3C (EC 3.4.22.28)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTECTION: TO STEED IN THE FOLDER THE THE PECE PROTEIN ATTACHES TO VESICULAR MEMBRANES AND IS ASSOCIATED WITH VIRAL RNA SYNTHESIS.

-!- SUBUNIT: THE VIRUS CAPEID IS COMPOSED OF 60 ICOSAMEDRAL UNITS, EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2, AND VP4.

-!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS. CLEAVAGE BETWEEN VP4 AND VP2 IS AUTOCATALYTIC; VP1/P2A IS CLEAVAGE BETWEEN VP4 AND VP2 IS AUTOCATALYTIC; VP1/P2A IS CAPALYZED BY P2A; ALL OTHER CLEAVAGES ANE CAPALYZED BY P3C.
-!- SIMILARITY: P2A PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
                                                                                                                                                                                                                       Coxsackievirus B1 (strain Japan).
Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
Enterovirus.
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDILINE-88122157; PubMed=3027969;
MEDILINE-88122157; Nomoto A.;
"Complete nucleotide sequence of the genome of coxsackievirus Bl.";
Virology 16:64-73 (1987).
-i- FUNCTION: P2A AND THE P3C POLYPEPTIDES ARE PROTEASES THAT CLEAVE
AT CERTAIN Q/G SITES IN THE POLYPROTEIN. THEY ARE CYSTEINE
                  2182 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cys-protease-3C.
                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pico_P2B.
RNA_helicase.
RNA_pol_P3D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pico_PlA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pico_P2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M16560; AAC00531.1; -.
                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002527; P
InterPro; IPR000605; R
InterPro; IPR001205; R
InterPro; IPR001676; R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000199;
InterPro; IPR003138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A26353; GNNYBL
HSSP; P03313; 1COV.
                                                                                                                                                                                                                                                                                NCBI_TaxID=103902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; C03.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEROPS; C03.022
                POLG_CXB1J
POLG_CXB1J
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PROSITE; PS00018; EF_HAND; 3
Calcium-binding; Repeat.
CA_BIND 16 27
CA_BIND 53 64
CA_LBIND 83 94
SEQUENCE 171 AA; 19687 MW
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420 4
572 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
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                                                                                           DR
FT
FT
SQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R Pfam; PF00548; Cys-prote.

JR Pfam; PF00548; Pico_PIA; 1.

DR Pfam; PF00325; Pico_PIA; 1.

DR Pfam; PF00152; Pico_PIA; 1.

DR Pfam; PF001015; Pico_PIB; 1.

DR Pfam; PF001015; NRA_dep_RNA_pol; 1.

DR ProDom; PD001125; Cys-protease-3C; 1.

DR ProDom; PF001125; Cys-protease-3C; 1.

DR ProDom; PF001125; Cys-protease-3C; 1.

DR ProDom; PD001125; Cys-protease-3C; 1.

DR ProDom; PF001125; Cys-protease-3C; 1.

DR ProDom; PF001126; Transferase; 1.

DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECURDARY STATES STRAIN-CHIRESE:
Clough K.A., Brindley P.J.;
Submitted (CCT-1995) to the EMBL/GenBank/DDBJ databases.
-!-SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, BELONGS
-:- TO THE SORCIN/GRANCALCIN/CALPAIN LIGHT CHAIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schistosoma japonicum (Blood fluke).
Bukaryota, Metazoa, Platyhelminthes; Turbellarian Platyhelminths;
Rhabditophora; Eulecithophora; Revertospermata; Mediofusata;
Rodermata; Trematoda; Digenea; Strigeidida; Schistosomatoldea;
Schistosomatidae; Schistosoma.
MCBI_TaxID=6182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SORCIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             846 TTTGAFGQQSGAVYVGNYRVVNRHLATREDWQRCV 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 TTVGVFG-----IEQDWDRCV 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P02593; IAK8.
InterPro; IPR0002048; EF-hand.
Pfam; PF00036; efhand; 4.
SMARI; SM00054; EFh; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U39069; AAB17908.1; -. HSSP; P02593; IAK8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SORC_SCHJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SORC_SCHJA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-ICR; TISSUE-Brain;
MEDLINE-9814466; pubMed-9652388;
MEDLINE-9814466; pubMed-9652388;
Byk T., Ozon S., Sobel A.;
"The Ulp family phosphoproteins -- common and specific properties.";
Eur. J. Biochem. 254:14-24(1998).
-- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
-- SIMILARITY: BELONGS TO THE DEHYDROPYRIMIDINASE FAMILY.
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hamajima N., Kato Y., Kouwaki M., Wada Y., Sasaski M., Nonaka M.; Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                          ó:
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
DDP4_MOUSE STANDARD; PRT; 572 AA.

AC 035098; 008886; DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 39, Last sequence update)
DE 10-HVDROPYRIMIDINASE RELATED PROTEIN-4 (DRP-4) (ULIP4 PROTEIN).
                                                                                                                                                                    Score 42; DB 1; Length 171;
Pred. No. 6.8;
2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.0%; Score 41; DB 1; Length 572; 47.4%; Pred. No. 35; tive 3; Mismatches 3; Indels
EF-HAND 1 (POTENTIAL).
EF-HAND 2 (POTENTIAL).
EF-HAND 3 (POTENTIAL).
251FB948FA07ADDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ER -> DG (IN REF. 2).
G -> V (IN REF. 2).
F -> I (IN REF. 2).
37671129FC02C7AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB006715; BAA218881; -.
EMBL; Y09079; CAA70299.1; -.
MGD; MGI:1349764; Dpys14.
InterPro: IPR002195; Dihydrooratase.
Pfam; PP00744; Dihydrooratase; 126 CONFLICT 125 126
   27 E1
64 E1
94 E1
19687 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420 F
61961 MW;
                                                                                                                                                             40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354 GVNGIEERMSVVWEKCVAS 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 47.48;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 GVFGIEQD----WDRCVIS 19
                                                                                                                                                                Query Match
Best Local Similarity 43.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                           1 NTTVGVFGIEQDWDRC 16
                                                                                                                                                                                                                                                                                                                           63 NEFLGLEKYVODWOTC 78
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m

342 STVTVLGITSDFYQCSIS 359

g

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                                                                                                                                                                                                                                           "Sequencing, genomic organization, and preliminary promoter analysis of a black cherry (R)-(+)-mandelonitrile lyase gene."; plant physiol. 115:1359-1369(1997).

Plant Physiol. 115:1359-1369(1997).

-- FUNCTION: INVOLVED IN CYANOGENIS, THE RELEASE OF HCN FROM INJURED TISSUES. CAPALYSES THE STEREOSPECIFIC ADDITION OF HCN TO A VARIETY OF ALDEHYDES IN VITRO. IS A MAJOR SEED CONSTITUENT, AND COULD HAVE THE ADDITIONAL ROLE OF A STORAGE FORM FOR REDUCED NITROGEN.

--- CAPALIZIC ACTIVITY: MANDELONITRILE = CYANIDE + BENZALDEHYDE.
                                                                                                                                                                                                                                                                                                                                                           SUBGULIT: MONOMER.
SUBCELLULAR LOCATION: PRIMARILY FOUND WITHIN PROTEIN BODIES OF THE COTLEDONARY PARENCHYMA CELLS WITH LESSER AMOUNTS WITHIN THE PROCAMBIUM (BY SIMILARITY).
SIMILARITY: BELONGS TO THE GMC OXIDOREDUCTASES FAMILY.
                                                                                                                                        Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Sperimatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Rosales; Rosaceae; Prunus.
NCBI_TAXID=23207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
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                                                             01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
(R)-MANDELONITRILE LYASE ISOFORM 3 PRECURSOR (EC 4.1.2.10)
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N-LINKED (GLCNAC.
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(GLCNAC...
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MEDLINE=98076189; PubMed=9414550;
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                                                                                                                             Prunus serotina (Black cherry).
                                                    (Rel. 34, Created)
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                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                   COFACTOR: FAD
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P52707;
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  RESULT 4
RESULT
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

Hu Z., Poulton J.E.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN CYANOGENIS, THE RELEASE OF HCN FROM INJURED
-!- FUNCTION: INVOLVED IN CYANOGENIS, THE RELEASE OF HCN TO A VARIETY
OF ALDEHYDES. CATALYSES THE REPERFORM OF HCN TO A VARIETY
OF ALDEHYDES IN VITRO. IS A MAJOR SEED CONSTITUENT, AND COULD HAVE
THE ADDITIONAL ROLE OF A STORAGE FORM FOR REDUCED NITROGEN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: MONOMER.
SUBCELLULAR LOCATION: PRIMARILY FOUND WITHIN PROTEIN BODIES OF THE
COTYLEDONARY PARENCHYMA CELLS WITH LESSER AMOUNTS WITHIN THE
                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
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PROSITE; PS00623; GMC_OXRED_1; 1.
PROSITE; PS00624; GMC_OXRED_2; 1.
Lvase; Glycoprotein; FAD; Flavoprotein; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (R)-MANDELONITRILE LYASE ISOFORM 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- CATALYTIC ÁCTIVITY: MANDELONITRILE = CYANIDE + BENZALDEHYDE
-!- COFACTOR: FAD.
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                                                                                                                                                                                  (EC 4.1.2.10)
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-!- SIMILARITY: BELONGS TO THE GMC OXIDOREDUCTASES FAMILY.
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N-LINKED (GLCNAC. .) (POT N-LINKED (GLCNAC
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35;
                                                                                                                               15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, ASE ISOFORM 2 PRECURSOR (HYDROXYNITRILE LYASE 2) (R)-OXYNITRILASE 2)
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                          Rosales; Rosaceae; Prunus.
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                                                      PRT;
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                                                                                                      (Rel. 37, Created)
                                                                                                                                                                                                                                                           Prunus serotina (Black cherry)
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                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=23207;
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                                                                                                      15-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDINE-22277665; Pubmed-1593641; Trewitt P.M., Heilmann L.J., Degrugillier S.S., Kumaran A.K.; Trewitt P.M., Heilmann L.J., Degrugillier S.S., Kumaran A.K.; "The boll weevil vitellogenin gene: nucleotide sequence, structure, and evolutionary relationship to nematode and vertebrate vitellogenin
     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genes.";
J. Mol. Evol. 34:478-492(1992).
-!- PUNCTION: PRECURSOR OF THE EGG-YOLK PROTEINS THAT ARE SOURCES OF
NUTRIENTS DURING EMBRYONIC DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                Anthonomus grandis (Boll weevil).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera; Endopterygota; Coleoptera; Polyphaga;
Cuculiformia; Phytophaga; Curculionidae; Curculioninae; Anthonomini;
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Pred. No. 1.4e+02;
2; Mismatches 2; Indels 1.
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     Indels
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 40, Last annotation update)
VITELLOGENIN PRECURSOR [CONTAINS: YP47; YP160]
                                                                                                                                                                                                                                   PRT; 1790 AA
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VITELLOGENIN.
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POTENTIAL.
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InterPro; IPR001747; Vitellogenin_N.
InterPro; IPR001846; Vwd.
Pfam; PF01347; Vitellogenin_N; 1.
Pfam; PF00094; Vwd; 1.
Glycoprotein; Storage protein; Signal.
SIGNAL 1 19
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larity 61.5%;
Conservative
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                                                     2 TTVGVFGIEQDWDRCVIS 19
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                                                                                                                                                                                                                                   VIT_ANTGR
Q05808;
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STRUCTURE BY IMR.
MEDILINE—88111667; PubMed—2892680;
Widmer H., Wagner G., Schweitz H., Lazdunski M., Wuethrich K.;
Widmer H., Wagner G., Schweitz H., Lazdunski M., Wuethrich K.;
"The secondary structure of the toxin ATX Ia from Anemonia sulcata in aqueous solution determined on the basis of complete
sequence-specific IH-NMR assignments.";
Eur. J. Biochem. 171:177-192(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRUCTURE BY NWR.
MEDILINE-90160299; PubMed-2576133;
Widmer H., Billeter M., Wusthrich K.;
"Three-dimensional structure of the neurotoxin ATX Is from Anemonia sulcata in aqueous solution determined by nuclear magnetic resonance spectroscopy.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THE MOLECULES)
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Proteins 6:357-371(1989).

Proteins 6:357-371(1989).

Proteins 6:357-371(1989).

Proteins 6:357-371(1989).

Proteins 6:357-371(1989).

Processes a structural substance of the sobium channel, Thereby Thurantary To OTHER SEA ANEMONE SODIUM CHANNEL INHIBITORY TOXINS. THIS IS A TYPE I TOXIN.

PIR: A01796; TAZAI.

PDB; LATX: 15-JUL-91.

InterPro; IRRO00693; Anenome_toxin.

Pram: Prof076; toxin_4; 1.

Toxin: Sodium channel, 4; 1.

Toxin: Sodium channel, 4; 1.

Possilis and 4 and 1 inhibitor; Multigene family; 3D-structure.
             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
NEUROTOXIN 1 (TOXIN ATT.1)
Anemonia sulcata (Shake-locks sea anemone).
BUKATOÇA: Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria; Mynantheae; Actiniidae; Anemonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                    MEDLINE-79024590; PubMed-29753;
Wunderer G., Bulliz M.;
"Amino-acid sequence of toxin I from Anemonia sulcata.";
Eur. J. Biochem. 89:11-17(1978).
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Pred. No. 3.7;
2; Mismatches (
46 AA.
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STANDARD;
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                                                                                                                                                                                                                                                                             STRAIN=DSM 1728;
MEDLINE-20479972; PubMed=11029001;
MEDPD A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
Mewes H. W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
"The genome sequence of the thermoacidophilic scavenger Thermoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structural conservation of the isolated zinc site in archaeal zinc-contenting ferredoxins as revealed by X-ray absorption spectroscopic analysis and its evolutionary implications."; J. Biol. Chem. 274:23160-23168(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                        Cosper N.J., Stalhandske C.M.V., Iwasaki H., Oshima T., Scott R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELECTRONS IN A WIDE VARIETY OF METABOLIC REACTIONS. COFACTOR: BINDS ONE 3FE-4S AND ONE 4FE-4S CLUSTER AND ONE ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Iwasaki T., Suzuki T., Kon T., Imai T., Urushiyama A., Ohmori D.,
                                                                                                                                                                                    Wakabayashi S., Fujimoto N., Wada K., Matsubara H., Kerscher L.,
Oesterhelt D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biol. Chem. 272:3453-3458(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:- MASS SPECTROMETRY: MW=15961; MW_ERR=10; METHOD=MALDI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPRO1450; 4FE4S_ferrdxin.
Pfam; PF00037; fer4; 2.
PROSTIF: PS00198; 4FE4S_FERREDOXIN; 1.
Electron transport; Iron-sulfur; Repeat; 4Fe-4S; 3Fe-4S; Zinc; COmplete proteome.

INIT_MET 0 0 ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oshima T.; "Novel zinc-containing ferredoxin family in thermoacidophilic
                                                                                                                                                                                                            "Amino acid sequence of a ferredoxin from thermoacidophilic archaebacteria, Thermoplasma acidophilum.";
FEBS Lett. 162:21-24(1983).
                                                                                                            Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmaceae; Thermoplasma.
                                               21-JUL-1986 (Rel. 01, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ZINC-CONTAINING FERREDOXIN.
           142 AA
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-15, AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99367440; PubMed-10438486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97166191; PubMed-9013590;
       FER_THEAC STANDARD; 1 P00218; Q9V304; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL445067; CAC12568.1; -. EMBL; AB023294; BAA82797.1; -.
                                                                                                                                                                                                                                                                                                                                                       Nature 407:508-513(2000).
                                                                                                Thermoplasma acidophilum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A00222; FEYTA.
HSSP; P55907; 1XER.
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                        STRAIN=DSM 1728;
                                                                                                                                     NCBI_TaxID=2303;
                                                                                   ZFX OR TA1448.
                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=HO-62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                            ZINC (PROBABLE).
ZINC (PROBABLE).
ZINC (PROBABLE).
ZINC (PROBABLE).
IRON-SULFUR 1 (3FE-4S) (PROBABLE).
IRON-SULFUR 1 (3FE-4S) (PROBABLE).
IRON-SULFUR 2 (4FE-4S) (PROBABLE).
IRON-SULFUR 1 (3FE-4S) (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Purayeuenis.";
J. Bacteriol. 176:3631-3637(1894).
-!- SIMILARITY: BELONGS TO THE FLAGELLA BASAL BODY ROD PROTEINS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 1; Length 142;
Pred. No. 12;
4; Mismatches 5; Indels
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E -> A (IN STRAIN HO-62).
0E1970A7FBDA07D5 CRC64;
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N-TERMINAL EXTENSION
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
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3; Mismatches
                            PERREDOXIN
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InterPro: IPR001444; Flag_bb_rod.
Pfam; PF004660; flg_bb_rod; 1.
PROSITE; PS00588; FLAGELLA_BB_ROD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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MEDLINE=94266716; PubMed=8206841;
                                                                                                                                                                                                                                                                                                                                                                                                          MM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 38.1%;
Best Local Similarity 38.9%;
Matches 7; Conservative
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101
105
142 AA;
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Best Local Similarity
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Q56326;
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01-NOV-1995 HXTD_YEAST P42833;

HXTD_YEAST

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TISSUE-Macrophage;
MEDILINE-9745441; PubMed-9355733;
BECCALI T., Appolloni M.G., Costanzi E., Stinchi S., Stirling J.L.,
Della Fazia M.A., Servillo G., Viola M.P., Orlacchio A.;
Lysosomal alpha-mannosidases of mouse tissues: characteristics of the
                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "I Neurosci 16:6197-6207(1996).

-! SUBCELLUAR LOCATION: CYTOPLASMIC (POTENTIAL).

-!- DEVELOPMENTAL STAGE: EXPRESSED TRANSIENTLY IN DEVELOPING SPINAL

-!- CORD AND SELECTIVELY IN THE POSTNATAL CEREBELLUM.

-!- SIMILARITY: BELONGS TO THE DEHYDROPYRIMIDINASE FAMILY.
                                                                                                                                                                           15-JUL-1998 (Rel. 36, Last sequence update)
Li-JUL-1998 (Rel. 36, Last annotation update)
DIHVDROPYRIMIDINASE RELATED PROFEIN-4 (DRP-4) (COLLAPSIN RESPONSE MEDIATOR PROTEIN 3) (CRMP-3) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse),
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
NCBL_raxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAZB_MOUSE STANDARD; PRT; 1012 AA.
009159; Q64443; O55037;
15-JUL-1998 (Rel. 36, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
ALYSOSOMAL ADPHA-MANNOSIDASE, PRECURSOR (EC 3.2.1.24) (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN).
MANZBI OR MANZB OR MANB OR LAMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang L., Strittmatter S.M.;
"A family of rat CRMP genes is differentially expressed in the
nervous system.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.1%; Score 40; DB 1; Length 564; 42.1%; Pred. No. 50; tive 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       564 AA; 61085 MW; 42050891CC1436D2 CRC64;
                                                                         564 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR002195; Dihydrooratase.
                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
MEDLINE=96424532; PubMed=8815901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002195; Dihydrooratas
Pfam; PF00744; Dihydrooratase; 1.
NON_TER
SEQUENCE 564 AA; 61085 MW; 420
                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U52103; AAB03281.1; -. HSSP; P18316; 1KRC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         346 GINGIEERMSVVWEKCVAS 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 GVFGIEQD----WDRCVIS 19
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Best Local Similarity 44...
Best Local Similarity 44...
                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nervous system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
MA2B_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | SEQUENCE FROM N.A. | SETAIN = STAIN = SEQUENCE FROM N.A. | STAIN = SEQUENCE FROM N.A. | STAIN = SEABLE / FY1676; | MEDLINE = 96076632; | PubMed = 7502583; | Maffabi M., nicaud J. - M., Levesque H., Gaillardin C.; | Maffabi M., nicaud J. - M., Levesque H., Gaillardin C.; | Maffabi M., nicaud J. - M., nown genes, a new member of the hexose transporter family and ten new open reading frames."; | Function: PROBABLE GLUCOSE TRANSPORTER. | FUNCTION: PROBABLE GLUCOSE TRANSPORTER | FAMILY. | SELONGS TO THE SUGAR TRANSPORTER FAMILY. | SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. | STAILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. | STAILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. | STAILARITY: | STA
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EMBL; Z71595; CAA96250.1; -
SGP; S0005262; HTV14.
SGP; S0005262; Sugar_trnsportr.
InterPro; IPR003662; Sub_trnsportr.
Pfan; PF00083; Sugar_tr; IPRANSPORT.
PRIMTS; PR00171; SUGAR_TRANSPORT.
PROSITE; PS00215; SUGAR_TRANSPORT_2; IFALSE_NEG.
PROSITE; PS00215; SUGAR_TRANSPORT_2; IRRANSPORT_2; IRRANSPORT_2;
                                                                                                                                                                                                                                                                                                                                                                   HXT14 OR HXT9 OR YNJ318C OR N0345.
Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyceteles;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
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91A68BA27099EEF8 CRC64;
                                                                                                                                                                                                                                    (Rel. 32, Created)
(Rel. 34, Last sequence update)
(Rel. 34, Last annotation update)
                                                                                                                                                                           540 AA.
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                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Las HEXOSE TRANSPORTER HXT14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 TVGVFGIEQDWDRCVI 18
                                                                                                                                                                               STANDARD;
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1168
1228
2264
3362
3362
4427
540
5523
113 TTAGAFGVDRD 123
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524
540 AA;
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Best Local Similarity
Matches 8; Conser
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TRANSMEM TRANSMEM TRANSMEM TRANSMEM TRANSMEM TRANSMEM

SEQUENCE

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Gaps

4;

DB 1; Length 1012; 92;

38.18; 47.18;

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Query Match 38.1
Best Local Similarity 47.1
Matches 8; Conservative
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MLTB_ECOLI
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                                                                                                                                                                                                                  Merkle R.K., Zhang Y., Ruest P.J., Lal A., Liao Y.-F., Moremen K.W.;
"Cloning, expression, purification, and characterization of the murine lysosomal acid alpha-mannosidase.";
lyosomal acid alpha-mannosidase.";
lyosomal acid alpha-mannosidase.";
lyocotim. Blophys. Acta 1385:132-146(1997).
-!- FUNCTION: NECESSARY FOR THE CATABOLISM OF N-LINKED CARBOHYDRATES RELEASED DURING GLYCOPROTEIN TURNOVER.
-!- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING ALPHA-D-MANNOSIDES.
                                                  SEQUENCE FROM N.A.
Stinchi S., Stirling J.L., Orlacchio A., Beccari T.;
"Promoter characterization and structure of the gene encoding mouse llysosomal alpha-mannosidase.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
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Hydrolase; Glycosidase; Glycoprotein; Lysosome; Zymogen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
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isoenzymes, and cloning and expression of a full-length cDNA."; Biochem. J. 327:45-49(1997).
                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: LYSOSOMAL.
-!- SIMILARITY: BELONGS TO FAMILY 38 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LYSOSOMAL ALPHA-MANNOSIDASE
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W; 4FE9EE5AED74709C CRC64;
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InterPro; IPR000602; Glyco_hydro_38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U29947; AAC53369.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF044190; AAC78560.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF044191; AAC78560.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U87240; AAC09470.1; ALT_INIT
                                                                                                                                                                               TISSUE=Liver;
MEDLINE=97449314; PubMed=9305783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114480 MW;
                                                                                                                                                                  SEQUENCE OF 3-1012 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
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CARBOHYD
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CONFLICT
SEQUENCE
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CARBOHYD
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-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-!- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE CYSTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=OH-1-P-CL1;
MEDLINE=95375238; PubMed=7647306;
METCHAR F., Kindle K.L., Llama M.J., Serra J.L., Fernandez E.;
Metchan F., Kindle K.L., Llama M.J., Serra J.L., Fernandez E.;
"Cloning and sequencing of the nitrate transport system from the thermophilic, filamentous cyanobacterium Phormidium laminosum: comparative analysis with the homologous system from Synechococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sp. PCC 7942.";
Plant Mol. Biol. 28:759-766(1995).
-!- FUNCTION: PROBABLY PART OF A HIGH-AFFINITY BINDING-PROTEIN-
DEPENDENT TRANSPORT SYSTEM FOR NITRATE; PROBABLY RESPONSIBLE THE TRANSLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
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                                                     7; Indels
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5BE86C4B02EFC5F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Cyanobacteria; Oscillatoriales; Phormidium.
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InterPro; IPR000515; BPD_transp.
Plam; PF00528; BPD_transp; 1.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transport; Transmembrane; Nitrate assimilation.
TRANSMEM 30 50 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                    01-NoV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
NITRATE TRANSPORT PERMEASE PROTEIN NRTB.
Score 40; DB 1
Pred. No. 92;
2; Mismatches
                                                                                                                                                                                                                                                                                                                 279 AA.
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715 TVGPIPVRDDWGKEVIS 731
                                                                                                              3 TVGVFGIEQDWDRCVIS 19
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Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                 STANDARD;
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217
249
279 AA;
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Q51881;
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RANGE STANDAR 
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                                                                Ol-FEB-1995 (Rel. 31, Created)
Ol-FEB-1995 (Rel. 31, Last sequence update)
Ol-FEB-1995 (Rel. 31, Last sequence update)
AGNG-2001 (Rel. 40, Last annotation update)
MEMBERANE-BOUND LIYLE WHEELY PRANSGIYCOSYLASE B PRECURSOR (EC 3.2.1.-)
(WURELN HYDROLASE B) (35 KDA SOLUBLE LYTIC TRANSGIXCOSYLASE) (SLT35).
ESCHERICHIA COli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PURAINELE CONTROL NO. 10. No. 
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MEDLINE-984347484, PubMed-9761817;
Van Asselt E.J., Perrakis A., Kalk K.H., Lamzin V.S., Dijkstra B.W.;
"Accelerated x-ray structure elucidation of a 36 kba
muramidase/transglycosylase using wARP.";
Acta Crystallogr. D 54:58-73(1998)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-RIZ / MG1657.
STRAIN-RIZ / MG1657.
STRAIN-RIZ / MG1657.
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Gragor J., Davis N.W., Kirkpatrick H.A., Godden M.A., Rose D.J., May B., Shao Y.;
Bu B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95309413; PubMed=7789526; Medikate A.J., Hermann F., Keck W.; "Cloning and controlled overexpression of the gene encoding the 35 kba soluble lytic transglycosylase from Escherichia coll."; FEBS Lett. 366:115-118(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=K12;
MEDLINE-96065704; PubMed=7476170;
Ehlert K., Hoeltje J.-V., Templin M.F.;
"Cloning and expression of a murein hydrolase lipoprotein from Escherichia coli.";
Mol. Microbiol. 16:761-768(1995).
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#PRELIMINARY SEQUENCE OF 1-91 FROM N.A.

#EDILINE-87194727; Pubmed-3553176;

#Gaucitol-specific enzymes of the phosphotransferase system in Escherichia coli. Waledetide sequence of the gut operon.";

J. Biol. Chem. 262:5455-5463(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-20035731; PubMed=10570954; Van Asselt E.J., Dijkstra B.W.; Wan Asselt E.J., Dijkstra B.W.; Ending of calcium in the EF-hand of Escherichia coli lytic transglycosylase Slt35 is important for stability."; FEBS Lett. 458:429-435(1999).
              361 AA
              PRT;
              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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W X-RXY CRYSTALLOGRAPHY (1.97 ANGSTROMS) OF 40-361.

W X-RXY CRYSTALLOGRAPHY (1.97 ANGSTROMS) OF 40-361.

W MEDLINE-20149813: PubMed-10684641;

Van Asselt E.J. Kalk K.H., Dijkstra B.W.;

"Crystallographic studies of the interactions of Escherichia coli
"Crystallographic studies of the interaction of Escherichia coli
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"Crystallographic studies of the Engres of the Escholarion and/or cell
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X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 40-361.
MEDLINE-20015368; PubMed=10545329;
Van Asselt E.J., Dijkstra A.J., Kalk K.H., Takacs B., Keck W.,
Dijkstra B.W.; Unikstra A.J., Kalk cell lytic transglycosylase streveals a lysosyme-like catalytic domain with an EF-hand.";
Structure 7:1167-1180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Ecogene; EG12699; mite.

PROSITE; PSOU013; PROKR_LIPOPROTEIN; 1.

PROSITE; PSOU013; PROKR_LIPOPROTEIN; 1.

Cell wall; Hydrolase; Glycosidase; Signal; Lipoprotein;

Outer membrane; Multigene family; 30-structure; Complete proteome.

SYGNAL 19 361 MEMBRANE:BOUND LYTIC MUREIN

TRANSGLYCOSTLASE B.

TRANSGLYCOSTLASE B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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Pred. No. 46;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40256 MW; 7E98F040504F75F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           371 AA.
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030207;
15-JUL-1998 (Rel. 36, Created)
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50.0%;
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162
361 AA;
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es 6; Conserv
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SEQUENCE
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Y028_ARCFU
ID Y028_AI
AC 030207;
DT 15-JUL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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DT 15-040-1998 (Rel. 36, Last sequence update)

DY ACCHAEGO (Rel. 40, Last annotation update)

CN ACCHAEGO (Rel. 40, Last annotation update)

SA Archaeoglobus fulgidus.

Archaeoglobus fulgidus.

Archaeoglobus fulgidus.

Archaeoglobus (Rel. 40, Last annotation update)

Archaeoglobus (Rel. 40, Last annotation (Rel. 40, Rel. 40, Rel. 41)

Archaeoglobus (Rel. 41, Rel. 41, Rel. 41, Rel. 41)

RA MEDITAXID-2234;

RA MEDITAXID-2234;

RA MEDITAN-VC16 / DSW 4304 / ARCC 49558;

RA MELHN -P. Clayton R.A. Town D.F. White O., Nelson K.E.,

RA MELHN R.A. Dodgon R.A., Town D.F. With the O., Nelson K.E.,

RA Klenk H.-P., Clayton R.A., Town D.-F., White O., Nelson K.E.,

RA Klenk H.-P., Clayton R.A., Town D.-F., Winte O., Nelson R.B.,

RA Richardson D.L., Kerlavage A., McKenney K., Suthan D., Lofton G., Cill S.,

RA Neterson S., Reich C.I., McHall L.K., Badger J.H., Glodek A., Shoth M. Saddw R.B., Verlave R.B., Bown D., Welmen S., Reich G.J., Fraser C.M., Smith H.O., Woese C.R., Shown C. C., Full C., Carland S.A.,

RA Neterson S., Reich G.J., Fraser C.M., Smith H.O., Woese C.R., Shown C. S., Cotton M.D., Spriggs T., Ariache P., Sown C., Fraser C.M., Smith H.O., Woese C.R., Shown C. S., Relax R. Saddw R. W., Olson G.J., Fraser C.M., Smith H.O., Woese C.R., Shith H.O., Shith H.O., Woese C.R., Shith H.O., Shith H.
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Search completed: March 14, 2002, 09:24:52 Job time: 908 sec.

4 VGVFGIEQDWDRCVI 18 : | | : : : | | : : | 217 IGVMGMKEEWAEIVL 231

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0; Gaps

Indels

Mismatches

37.1%; nilarity 33.3%; Conservative

Query Match Best Local Similarity Matches 5; Conserv

Score 39; DB 1; Length 371; Pred. No. 48;

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

March 14, 2002, 09:10:44; Search time 56.96 Seconds Run on:

(without alignments)
25.409 Million cell updates/sec

105 1 NTTVGVFGIEQDWDRCVIS 19 US-09-765-739A-5 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir1:* pir2:* pir3:* pir4:* PIR_68:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result		Query				
NO.	Score	Match	Match Length	BB	ΩI	Description
г	105	100.0	286	7	JE0219	28k surface antige
7	11	73.3	280	7	JE0217	
æ	73	69.5	276	~	JE0218	
4	51	48.6	278	7	JE0216	28k surface antige
വ	47	44.8	160	7	A75466	ω
9	46		284	7	140882	major antiqenic pr
7	44.5		2182	Н	GNNYB1	qenome polyprotein
ω	43		5188	~	B85547	probable RTX famil
σ	42.5		417	7	E84430	probable inositol
10	42	40.0	244	~	E84885	hypothetical prote
11	41	39.0	142	~	F83359	
12	41	39.0	299	~	S68198	probable transcrip
13	41	39.0	573	~	T07948	mandelonitrile lya
14	41	39.0	576	7	T08073	mandelonitrile lya
15	41	39.0	688	~	JC2248	polyprotein - swee
16	40.5	38.6	202	7	A72479	hypothetical prote
17	40.5	38.6	1790	-	S27772	vitellogenin precu
	40	38.1	46	П	TZA21	toxin I - snake-lo
19	40	38.1	143	-	FEYTA	ferredoxin [3Fe-4S
20	40	38.1	349	7	F70357	lipoprotein - Aqui
21	40	38.1	361	7	C85430	MAP kinase like pr
22	40	38.1	398	7	C83499	probable transglyc
23	40	38.1	436	~	T28066	hypothetical prote
24	40	38.1	530	7	T23255	hypothetical prote
25	40	38.1	540	7	S63299	sugar transport pr
. 56	40	38.1	1012	7	T42385	alpha-mannosidase
	40	38.1	1090	7	C86577	PBP2-transglycolas
28	40	38.1	1090	7	D72048	pbp2-transglycolas
29	39.5	37.6	116	~	T36999	probable transposa

unknown protein en probable positive	nitrate transport probable ribf prot	membrane-bound lyt membrane-bound lyt membrane-bound lyt	conserved hypothet acetyltransferase gene P2X3 protein	purinoceptor P2X - hypothetical prote probable short-cha	probable phenylala mandelonitrile lya
B85712 T43123	536842 A70884 T44902	A65050 B85918 H83088	D69253 F69008 I58099	S60334 D84751 T40997	E72457 T50766
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265	331	361 361 367	371 377 397	397 462 503	548 574
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30 31	333	35 37	38 39 40	4 4 4 3 2 5 6	44 45

ALIGNMENTS

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Nighternate names: MAP1
C; Species: Ehrlichia chaffensis)
C; Species: Ehrlichia chaffensis)
C; Species: 21-aug-1998 #sequence_revision 21-aug-1998 #text_change 17-Mar-1999
C; Accession: JE0219
R; Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R. Biochem. Biophys. Res. Commun. 247, 636-643, 1998
A; Tible: Molecular characterization of a 28kDa surface antigen gene family of the tri A; Reference number: JE0216; MUID:98321180
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                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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0
                                                                                                                                                                                                                                                                                                                                     Length 286;
                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                     Score 105; DB 2;
Pred. No. 1.1e-09;
; Mismatches 0;
- Ehrlichia chaffensis
                                                                                                                                                                                                                                                                                                                       100.0%; Scor
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 NTTVGVFGIEQDWDRCVIS 78
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NTTVGVFGIEQDWDRCVIS 19
                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-286 <RED>
A;Cross-references: GB:AF062761
                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 19; Conservative
súrface antigen 2
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28k surface antigen 4 - Ehrlichia chaffensis
28k surface antigen 4 - Ehrlichia chaffensis
N.Alternate names: MAP1
C.Speciaes: Ehrlichia chaffensis
C.Speciaes: Comun. 2017
R.Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R. Biochem. Biophys. Res. Commun. 247, 636-643, 1998
A;Title: Molecular characterization of a 28kDa surface antigen gene family of the tri
A;Reference number: JE0216; MUID:98321180
A;Residues: J-280 <RED>
A;Residues: 1-280 <RED>
A;Residues: 1-280 <RED>
A;Cross-references: GB:AF062761

Query Match 73.3%; Score 77; DB 2; Length 280; Best Local Similarity 68.4%; Pred. No. 4.4e-05; Matches 13; Conservative 3; Mismatches 3; Indels 1 NTTVGVFGIEQDWDRCVIS 19 οy

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Gaps

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60 NTTIGVFGLKQDWDGSTIS 78 qq

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GNNYBI

GNNYBI

GNNYBI

GNNYBI

GNNYBI

N.Contains: coat protein 1A; coat protein 1B; coat protein 1D; core
N.Contains: coat protein 1A; coat protein 1B; coat protein 1D; core
N.Contains: coat protein 1A; coat protein 1B; coat protein 1D; core
Dolymerase (EC 2, 7, 7, 48)

C; Species: coxsackievirus B1

C; Species: oxsackievirus B1

C; Species: oxsackievirus B1

C; Accession: A26533

R; Iizuka, N.; Kuge, S.; Nomoto, A.

Yirology 156, 64-73, 1987

A; Title: Complete nucleotide sequence of the genome of coxsackievirus B1.

A; Reference number: A26353; MUID: 87122157

A; Reference contains CRNA

A; Residuance number: A26353

A; Molecule type: genomic RNA

A; Residual type: genome polyprotein
C; Superfamily: poliovirus protein 1D #status predicted <PID>
F; 313-570-Product: coat protein 1D #status predicted <C2D>
F; 1427-155/Product: coat protein 2B #status predicted <C2D>
F; 1427-155/Product: core protein 2B #status predicted <C2D>
F; 1427-155/Product: core protein 2B #status predicted <C2D>
F; 1427-155/Product: core protein 3A #status predicted <PID>
F; 1427-155/Product: protein 3A #status predicted <PID>
F; 1427-155/Product: protein 3A #status predicted <PID>
F; 1538-1720/Product: protein 3A #status predicted <PID>
F; 1538-1720/Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.0882

14.0882

14.0882

C) Species: Cowdria ruminantium (heartwater rickettsia)

C) Accession: 140882; 842827

E) Van Vilet. AH. Jongejan, F.; van Kleef, M.; van der Zeijst, B.A.

Infect. Immun. 62, 1431-1456, 1994

A) Reference number: 140882; MUID:94178956

A) Status: preliminary; translated from GB/EMBL/DDBJ

A) Residues: 1-284 - REES

A) Cross-references: EMBL:X74250; NID:9454266; PIDN:CAA52309.1; PID:9454267

A) Genetics:
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Pred. No. 5.5;
3; Mismatches 2; Indels
                                                                                                                                                                              DB 2; Length 160;
                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                              Score 47; DB
Pred. No. 2.1;
4; Mismatches
                                                                                                                                                                              44.88;
46.78;
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                                                                                                                           Query Match
Best Local Similarity 46.7
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Best Local Similarity 58.3
Matches 7; Conservative
C; Keywords: methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                    4 VGVFGIEQDWDRCVI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 TVGVFGIEQDWD 14
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63 TKAVFGLKKDWD 74
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GNNYB1
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A Residues: 1-160 <WH>
A Residues: 1-160 <WH
A
                                                                                    28k surface antigen 5 - Ehrlichia chaffensis
NiAlternate names: MAP1
NiAlternate names: MAP1
Sible State: 21-Mar-1998
Sible State: 21-Mar-1999
Sible State: 247, 636-643, 1998
Airlie State: Marcasterization of a 28kDa surface antigen gene family of the tribe Airlie State: DNA
Airlie State: Sta
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Ni Alternate names: MAP1
(Species: Brhlichia chaffensis
C; Date: 21-Mag-1998 #catenee_revision 21-Aug-1998 #text_change 17-Mar-1999
(Species: 21-Mag-1998 #sequence_revision 21-Aug-1998 #text_change 17-Mar-1999
(Species: 21-Mag-1998 #sequence_revision 21-Aug-1998 #text_change 17-Mar-1999
(Species: Brochen: Biophys Res. Commun. 247, 636-643, 1998
A; Fleddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Biochem: Biophys. Res. Commun. 247, 636-643, 1998
A; Title: Molecular characterization of a 28KDa surface antigen gene family of the tribe A; Recession: JE0216
A; Recession: JE0216
A; Residues: 1-278 < RED>
A; Residues: 1-278 < RED>
A; Cross-references: GB:AF062761
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69.5%; Score 73; DB 2; Length 276;
Best Local Similarity 68.4%; Pred. No. 0.0002;
Matches 13; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Length 278;
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Pred. No. 0.82;
5; Mismatches
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Ouery Match 48.6%; Best Local Similarity 50.0%; Matches 7; Conservative

Op ολ

Óγ Ω DB 1; Length 2182;

42.48; Score 44.5;

Query Match

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hypothetical protein PA2282 [imported] - Pseudomonas aeruginosa (strain PAO1)
C; Species: Pseudomonas aeruginosa
C; Species: Pseudomonas aeruginosa 31-Dec-2000
C; Accession: F83359
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pa A; Reference number: A82950; MUID: 20437337
A; Accession: F83359
A; Accession: F83359
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-142 < STO>
A; Cross-references: GB: AE004654; GB: AE004091; NID: 99948311; PIDN: AAG05570.1; GSPDB: GK
C; Genetics:
A; Gene: PA2282
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: E84885
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Mierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487
A;Reference number: A84420; MUID:20083487
A;Residues: L-244 <STO>
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C;Genetics:
A;Gene: At2945010
A;Map position: 2
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A;Residues: 1-299 <BOT>
A;Cross-references: EMBL:Z21955; NID:g577589; PIDN:CAA79965.1; PID:g577593
R;Botella, J.A.; Murillo, F.J.; Ruiz-Vazquez, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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pred. No. 18;
3; Mismatches 3; Indels
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22;
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Pred. No.
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Best Local Similarity 50.0
Matches 6; Conservative
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61 NWTTGIFGCAEDPESC 76
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62 VEGLDHDWDRLI 73
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Best Local Similarity
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A;Cross-references: GB:AE005174; NID:g12513368; PIDN:AAG54838:1; GSPDB:GN00145; UWGP:206
A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable inositol polyphosphate-5-phosphatase [imported] - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: E84430
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; euss, D.; Merman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.A.; Reference number: A84420; MUID:20083487
A;Accession: E84430
A;Accession: E84430
A;Accession: E84430
A;Accession: E84430
A;Accession: E84420; MUID:20083487
A;Accession: E84430
A;Accession
                                                                                                                                                                                                                                                                                                                                                                                                                                               C:Species: Escherichia coli
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C:Accession: B85547
C:Accession: B85547
C:Accession: B85547
C:Accession: E.J. Dunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayheviller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
                                                                              ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                  Gaps
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                                                                              19;
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E84885
hypothetical protein At2g45010 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 5188;
                                                                              Indels
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Pred. No. 3.4e+02;
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                                                                                                                                                                                                            Score 42.5; DB Pred. No. 31; 3; Mismatches
                                                                                                                                                            ---IEQDWDRCV 17
                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                  Pred. No.
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50.0%;
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                                                                          Conservative
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Best Local Similarity
Matches 8; Conserv
                              Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
                                                                                                                                                            TTVGVFG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: At2g01900
A; Map position: 2
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Gaps

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Indels

Length 576;

Score 41; DB 2; Pred. No. 76; 3; Mismatches

potato feathery mottl

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RESULT 15
JO2248

DOIYPOTCH S. Sweet potato feathery mottle virus (fragment)
N;Contains: coat protein; nuclear inclusion b protein
C;Species: sweet potato feathery mottle virus
C;Species: sweet potato feathery mottle virus
C;Species: weet potato feathery mottle virus
C;Species: weet potato feathery mottle virus
C;Species: weet potato feathery mottle
C;Species: Word 1985 #sequence_revision 07-oct-1994 #text_change 17-Nov-2000
C;Accession: JC248, F0216
Biosci Biochechnol. T: Hayash, T: Nishiguchi, M.
Biosci Biochechnol. Biochem 58, 965-967, 1994
A;Title: Nucleotide sequence at the 3'-terminal region of sweet potato feath
A;Reference number: JC2248; MUID:94289871
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Job time: 361 sec
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Best Local Similarity 47.1%;
Matches 8; Conservative
      Query Match
Best Local Similarity 50.0%;
Matches 9; Conservative
                                                                                                                                                            :|| | || |: :| || || 343 STVTVLGITSDFYQCSIS 360
                                                                                                                          2 TTVGVFGIEQDWDRCVIS 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mandelonitrile lyase (EC 4.1.2.10) 3 - black cherry
C;Species: Prunus serotina (black cherry)
C;Species: Prunus serotina (black cherry)
C;Accession: T07948 #sequence_revision 21-May-1999 #text_change 17-Mar-2000
C;Accession: T07948 #sequence_revision 21-May-1999 #text_change 17-Mar-2000
C;Accession: T07948 #sequence_revision 21-May-1999 #text_change 17-Mar-2000
C;Accession: T07948 #sequence_revision (R)-(+)-mandelonitrile lyase isoform MDL3 precursor, mRNA
A;Resference number: 216239
A;Accession: T07948
A;Accession: T07948
A;Accession: T07949
A;Accession: T0794
A;Accession: T0794
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ArTitle: A cluster of structural and regulatory genes for light-induced carotenogenesis A; Reference number: S67950; MUID:96061955
A; Accession: S67958
A; Status: nucleic acid sequence not shown
A; Molecule type: DNA
A; Residues: 7-68 < NOW>
A; Cross-references: EMBL: 221955
C; Keywords: DNA binding
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39;
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Pred. No. 76;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                   Score 41; DB
Pred. No. 39;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                   39.0%;
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50.0%;
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Best Local Similarity 50.0
Matches 9; Conservative
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Best Local Similarity 66.7
Matches 8; Conservative
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284 VHVFQGEEDWDR 295
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Gaps

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7; Indels

Score 41; DB 2; Pred. No. 91; 2; Mismatches

Length 688

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

March 14, 2002, 09:07:40; Search time 54.54 Seconds Run on:

(without alignments)
7.839 Million cell updates/sec

Title:

US-09-765-739A-5 105 1 NTTVGVFGIEQDWDRCVIS 19 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

212252 seqs, 22503292 residues Searched:

212252 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Issued_Patents_AA:* Database :

1: /cgg2_6/ptcdata/2/laa/5A_COMB.pep:*
2: /cgn2_6/ptcdata/2/laa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/2/laa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/2/laa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/2/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptcdata/2/laa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

IES	Description	5 Sequence	7 Sequence 17,	-326-18	-230-4 Sequence 4, 1	-326-4 Sequence 4,	-326-16	Sequence 2,	Sequence 2,	5 Sequence 5,	Sequence	Sequence 9,		5 Sequence 16,	Sequence 17,		Sequence 7,	Sequence 2,	B-2 Sequence 2,	-2 Sequence 2,	3 Sequence 3,	-8 Sequence 8,	7 Sequence 7,	16	-165-3 Sequence 3,	-165-5 Sequence 5,	1,	22
SUMMARIES	ID	US-08-953	3	-08 - 953	-08-733	-08-953	-08 - 953	US-08-733	US-08-953-326-	US-08-808	US-09-306-902A	US-08-750	US-09-363-745-9	US-09-191	US-09-191	US-08-808-982-7	0S-09-306	US-08-072	-08-719	-09-092	US-08-945	PCT-US95-04801	US-08-431	US-09-347	US-08-586	-08-586	US-08-742	US-09-191
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de	Query Match	100.0	73.3	σ	69.5	69.5	48.6		41.9	41.9	41.9	37.1	37.1	37.1	37.1	37.1	37.1	37.1	37.1	37.1	35.7	35.2	35.2	35.2	35.2	35.2	35.2	35.2
	Score	105	77	73	73	73	51	44	44	44	44	39	39	39	39	39	39	39	39	m	37.5	37	37	37	37	37	37	37
	Result No.	7	7	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

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36 36 37 37 37 37 37 37 37 37 37 37 37 37 37	36 35.5
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### ALIGNMENTS

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; pracent No. 621872

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Barbet, Anthony F.
APPLICANT: Ganta, Roman R.
APPLICANT: Ganta, Aceme
APPLICANT: Nyika, Aceme
APPLICANT: Nyika, Aceme
APPLICANT: Nyika, Aceme
APPLICANT: Nyika, Aceme
APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
TITLE OF INVENTION: Animals and Humans
FILE REFERENCE: UF-16701
CURRENT APPLICATION NUMBER: US/08/953,326
EARLIER RAPLICATION NUMBER: 08/733,230
EARLIER PLIING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-17
SEQIID NOS: 24
SSOID NO 15
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100.0%; Pred. No. 2.1e-09;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-953-326-17
Sequence 17, Application US/08953326
Sequence 17, Application US/08953326
GENERAL INFORMATION:
APPLICANT: Barbet, Anthony F.
APPLICANT: Ganta, Roman R.
APPLICANT: Barcing, Travis C.
APPLICANT: Burridge, Michael J.
APPLICANT: Nyika, Aceme
APPLICANT: Rurangirwa, Fred R.
; Sequence 15, Application US/08953326; Patent No. 6251872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 286
7 TYPE: PRT
OKGANISM: Ehrlichia chaffeensis
US-08-953-326-15
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Best Local Similarity 100.
Matches 19; Conservative
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APPLICANT: Ganta, Roman Reddy
APPLICANT: McGulre, Travis C.
APPLICANT: Burridge, Michael J.
APPLICANT: Burridge, Michael J.
APPLICANT: Rurangirwa, Fred R.
APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Nucleic Acid Vaccines Against
TITLE OF INVENTION: Rickettsial Diseases and Methods of Use
NUMBER OF SEQUENCE: 6 CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREDT: 2421 NW. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                     COMPUTER: FLAPPY disk
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: US/08/733,230
CLASSIFICATION: 514
ATTORNEY/AGBNT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF-167
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 280 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-733-230-4
                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
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APPLICANT: Mahan, Suman M.

TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of FILE REPERENCE: UP-16701
CURRENT APPLICATION NUMBER: US/953,326
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1996-10-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 17
LENGTH: 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
69.5%; Score 73; DB 4; Length 276;
Best Local Similarity 68.4%; Pred. No. 0.0027;
Matches 13; Conservative 3; Mismatches 3; Indels
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(S-08-953-326-18
Sequence 18, Application US/08953326
Patent No. 6251872
GENERAL INFORMATION F.
                                                                                                                                                                                                                                                                                          TYPE: PRT
; ORGANISM: Ehrlichia chaffeensis
US-08-953-326-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Ehrlichia chaffeensis
US-08-953-326-18
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Sequence 4, Application US/08953326

Patent No. 6251872

GENERAL INFORMATION:
APPLICANT: Barbet, Anthony F.
APPLICANT: Garte, Roman R.
APPLICANT: Buridge, Michael J.
APPLICANT: Buridge, Michael J.
APPLICANT: Wish, Acemen
APPLICANT: Wahan, Suman M.
TITLE OF INVENTION: Mucleic Acid Vaccines Against Rickettsial Diseases of TITLE OF INVENTION: Annuals and Humans
FILE REFRENCE: UF-167C1
CURRENT APPLICATION NUMBER: US/08/953,326
CURRENT FILING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1996-10-17
SEARLIER FILING DATE: 1996-10-17
SOFTWARE: PALCATION NUMBER: 08/733,230
                                                           ö
                                                              Gaps
                                                        ;
0
Ouery Match 69.5%; Score 73; DB 3; Length 280; Best Local Similarity 68.4%; Pred. No. 0.00028; Matches 13; Conservative 3; Mismatches 3; Indels
                                                                                                                                         60 NTTVGVFGLKQNWDGSAIS 78
                                                                                                             1 NTTVGVFGIEQDWDRCVIS 19
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RESULT 4
US-08-733-230-4
Sequence 4, Application US/08733230
Fatent No. 6025338
GENERAL INFORMATION:
APPLICANT: Barbet, Anthony F.

```
Sequence 2, Application US/08953326

Betent No. 6251872

GENERAL INFORMATION:

APPLICANT: Barbet, Anthony F.

APPLICANT: Ganta, Roman R.

APPLICANT: McGuire, Travis C.

APPLICANT: McGuire, Travis C.

APPLICANT: McGuire, Travis C.

APPLICANT: Murangirwa, Fred R.

APPLICANT: Manany Suman M.

TITLE OF INVENTION: Animals and Humans
FILE REFERENCE: UF-16701

CURRENT APPLICATION NUMBER: US/08/953,326

CURRENT FILING DATE: 1997-10-17

EARLIER APPLICATION NUMBER: 08/953,326

EARLIER FILING DATE: 1997-10-17

EARLIER FILING DATE: 1997-10-17

WUMBER OF SEQ ID NOS: 24
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Pred. No. 13;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44; DB 3; Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.
                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
RERERENCE/DOCKET NUMBER: UF-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               287 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-733-230-2
                                                                                                                  COMPUTER READABLE FORM:
        Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 TVGVFGIEQDWD 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ||||:::|||
| 63 TQTVFGLKKDWD 74
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           STATE: FL
STATE: FL
COUNTRY: USA
32606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-953-326-2
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LENGTH: 287
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## Sequence 16, Application US/08953326

## Patent No. 6251872

## Patent No. 6251872

## PAPLICANT: Barbet, Anthony F.

## APPLICANT: Barbet, Anthony F.

## APPLICANT: Barridge, Michael J.

## APPLICANT: Burridge, Michael J.

## APPLICANT: Burridge, Michael J.

## APPLICANT: Wish, Aceme

## APPLICANT: Wish, Aceme

## APPLICANT: Wish, Aceme

## APPLICANT: Wish, Aceme

## APPLICANT: Wish, Fred R.

## APPLICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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APPLICANT: Rurangirwa, Fred R.
APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Nucleic Acid Vaccines Against
TITLE OF INVENTION: Rickettsial Diseases and Methods of Use
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 51; DB 4; Length 278;
Pred. No. 0.92;
5; Mismatches 2; Indels
                                                                                                                                                                                                 69.5%; Score 73; DB 4; Length 280; 68.4%; Pred. No. 0.00028;
                                                                                                                                                                                                                                                            3; Indels
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2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                         3; Mismatches
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Patent No. 6025338
GENERAL INFORMATION:
APPLICANT: Barbet, Anthony F.
APPLICANT: Ganta, Roman Reddy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ganta, Roman Reddy
APPLICANT: McGuire, Travis C.
APPLICANT: Burridge, Michael J.
                                                                                  ) ORGANISM: Ehrlichia chaffeensis
US-08-953-326-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Ehrlichia chaffeensis
US-08-953-326-16
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                                                                                                                                                                                                                                                                                                           1 NTTVGVFGIEQDWDRCVIS 19
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 50...
7; Conservative
                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                         Best_Local Similarity
Matches 13; Conserv
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SEQ ID NO 4
LENGTH: 280
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                                                                                                                                                                                                    Query Match
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Pred. No. 45;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PAX RECEPTORS (PURINOCEPTOR FAMILY)
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGIANA
STAFE: VIEGINIA
STAFE: VIEGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER RADABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/306,902A
FILING DATE: 07-May-1999
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/750,134A FILLIG DATE: 22-34N-1997 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
RECISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC96-217
TELECOMMUNICATION INFORMATION:
TELEFAN: (415) 343-4341
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 898 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: peptide
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-306-902A-5
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NAME: CRAMFORD, ARTHUR C.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 1430-116
TELECOMMUNICATION INFORMATION:
TELECHONE: (703) 816-4006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-08-750-134A-9
US-08-750-134A-9
Sequence 9, Application US/08750134A
Patent No. 5985603
Fatent No. 5985603
FAPLICANT: VALERA, SOLEDAD
APPLICANT: BUELL, GARK
APPLICANT: BUELL, GARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (703) 816-4100 INFORMATION FOR SEQ ID NO:
                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/09306902A

Patent No. 6277585

GENERAL INFORMATION:
GENERAL INFORMATION:
Leonardo, E. David
Hink, Lindsay
Masu, Masayuki
Kazuko, Keino-Masu
TITLE OF INVENTION: Netrin Receptors
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 268 BUSH STREET, SUITE 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
CONDUTER:
CONDUT
                                                                                                                                                       Sequence 5, Application US/08808982

Sequence 5, Application US/08808982

Patent No. 5939271

GENERAL INFORMATION:
APPLICANT: Henk, Landsay
APPLICANT: Hink, Lindsay
APPLICANT: Masu, Masayuki
APPLICANT: Razuko, Keino-Masu
TITLE OF INVENTION: Netrin Receptors
NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SS: not relevant
not relevant
E: peptide
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Best Local Similarity 58.3
Matches 7; Conservative
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| |||:::|||
63 TQTVFGLKKDWD 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: no
; MOLECULE TYPE:
US-08-808-982-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-306-902A-5
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qq ò

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APPLICANT: Abbort Laboratories
APPLICANT: Abbort Laboratories
APPLICANT: Lynch, Kevin J.
APPLICANT: Burgard, Edward C.
APPLICANT: Burgard, Edward C.
APPLICANT: Burgard, Edward C.
APPLICANT: Burgard, Edward C.
APPLICANT: Van Biesen, T.
TITLE OF INVENTION: Nucleic Acids Encoding A Functional
TITLE OF INVENTION: Human Purinoreceptor P2X3 and P2X6 And Methods Of Production
TITLE OF INVENTION: And Use Thereof
FILE REFERENCE: 6293 US.P1
CURRENT APPLICATION NUMBER: US 09/008,526
EARLIER APPLICATION NUMBER: US 09/008,185
EARLIER FILING DATE: 1998-01-16
SEARLIER FILING DATE: 1998-01-16
NUMBER OF SEQ ID NOS: 32
SOOFTWARE: FESTESC for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Abbort Laboratories
APPLICANT: Abbort Laboratories
APPLICANT: Lynch, Kevin J.
APPLICANT: Burgard, Edward C.
APPLICANT: Burgard, Edward C.
APPLICANT: Burgard, Edward C.
APPLICANT: Wan Biesen, T.
TITLE OF INVENTION: Human Purinoreceptor P2X3 and P2X6 And Methods Of Production
TITLE OF INVENTION: Human Purinoreceptor P2X3 and P2X6 And Methods Of Production
TITLE OF INVENTION: Human Purinoreceptor P2X3 and P2X6 And Methods Of Production
TITLE OF INVENTION: Human Purinoreceptor P2X3 and P2X6 And Methods Of Production
TITLE OF INVENTION: Human Purinoreceptor P2X3 and P2X6 And Methods Of Production
TITLE OF INVENTION NUMBER: US 09/008,526
EARLIER PLILING DATE: 1998-01-16
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NOS: 32
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8;
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Pred. No. 1.1e+02;
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Pred. No. 1.1e+02;
4; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17, Application US/09191136B Patent No. 6214581
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235 TGGVLGIKIGWVCDLDKAWDQCI 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.18;
34.88;
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34.8%;
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Best Local Similarity 34.00
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US-09-191-136-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
US-09-191-136-16
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                              Length 397;
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Pred. No. 1.1e+02;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-09-363-745-9
; Sequence 9, Application US/09363745
; Patent No. 6194162
; GENERAL INFORMATION:
APPLICANT: VALERA, SOLEDAD
APPLICANT: BUELL, GARY
; TITLE OF INVENTION: P2x RECEPTORS (PURINOCEPTOR FAMILY);
NUMBER OF SOUTENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: NIXON 6 VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZID: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/09/363,745
FILING DATE:
                                                                                                                                                                                           Score 39; DB 2; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: CRAWFORD, ARTHUR C.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 1430-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
INFORMATION FOR SEQ. ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
US-09-191-136-16
; Sequence 16, Application US/09191136B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/750,134
                                                                                                                                                                                                                                                                                                                     235 TGGVLGIKIGWVCDLDKAWDQCI 257
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Best Local Similarity 34.8%;
Matches 8; Conservative
                                                                                                                                                                                         Query Match 37.1%;
Best Local Similarity 34.8%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 397 amino acids amino acid
SEQUENCE CHARACTERISTICS
                                                                                      MOLECULE TYPE: protein
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                                             amino acid
                                                                         linear
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                                                                  TOPOLOGY:
                                                                                                                  US-08-750-134A-9
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3 TVGVFGI------EQDWDRCV 17

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REGULT 15

SQUERCE OF APPLICATION US/0808982

SQUERCE OF APPLICANT Exeritation US/0808982

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PRICAMIT HESTSTECT-LANGEN WASH, MARSH, MARSH, MARSH, MASH, M
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Search completed: March 14, 2002, 09:07:41 Job time: 842 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. OM protein - protein search, using sw model	on: March 14, 2002, 09:09:37 ; Search time 111.55 Seconds (without alignments) 12.617 Million cell updates/sec	Title: US-09-765-739A-5 Perfect score: 105 Sequence: 1 NTTVGVFGIEQDWDRCVIS 19	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	ched: 522463 seqs, 74073290 residues	Total number of hits satisfying chosen parameters: 522463	Minimum DB seq length: 0 Maximum DB seq length: 2000000000
OM prot	Run on:	Title: Perfect se Sequence:	Scoring	Searched:	Total	Minimu Maximu

A_Geneseq_1101:* Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA1986.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA1989.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA1991.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA1991.DAT:* /SIDS8/gcgdata/geneseq/genesegp/AA2000.DAT:*/SIDS8/gcgdata/geneseg/genesegp/AA2001.DAT:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Ehrlichia chaffeen	E. chafeensis OMP-	Ehrlichia chaffeen	Variable surface a	Ehrlichia chaffeen	Ehrlichia chaffeen	Variable surface a	E. chafeensis OMP-	E. chafeensis p28	Ehrlichia chaffeen	Ehrlichia chaffeen	
ΙD		AAY06946	AAB36186	AAU04196	AAW51094	AAB36188	AAU04198	AAY06948	AAY06942	AAW51095	AAB36189	
DB	19	20	21	22	19	21	22	20	20	19	21	
% Query e Match Length DB I	286	286	286	286	280	280	280	280	256	276	276	
% Query Match	100.0	100.0	100.0	100.0	73.3	73.3	73.3	70.5	69.5	69.5	69.5	
Score	105	105	105	105	77	77	77	74	73	73	73	
Result No.	1	7	3	4	2	9	7	80	6	10	11	

McGuire TC;

Mahan SM,

Ganta RR,

Barbet AF, Śurridge MJ, Nyika A, Rurangirwa FR; ) UNIV FLORIDA.

WPI; 1998-251232/22. N-PSDB; AAV07179.

EX EE

73 69.5 276 22 AAA 73 69.5 280 19 AAA 73 69.5 280 19 AAA 73 69.5 280 280 20 AAA 69.5 280 280 20 AAA 62 59.0 280 21 AAA 62 59.0 280 21 AAA 62 59.0 280 21 AAA 64 62 51.4 276 20 AAA 64 62 51.4 276 20 AAA 64 62 62 287 21 AAA 64 62 62 287 21 AAA 64 62 62 62 62 62 62 62 62 62 62 62 62 62	Variable surface a Ehrlichia chaffeen Ehrlichia chaffeen Major antigenic pr E. canis P30-2 pro Ehrlichia canis im Ehrlichia canis im Ehrlichia canis im E. canis P30-1 pro E. chafeensis OMP-		on; VSA2; rickettsia;
73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 74 41.9 74 41.9 74 41.9 74 41.9 74 41.9 74 41.9 75 74 70.0 75 75 75 75 75 75 75 75 75 75 75 75 75 7	AAV04199 AAB36183 AAV060943 AAY069943 AAY06952 AAY1477 AAY06961 AAY06961 AAY06961 AAY06961 AAY06961 AAY06961 AAY06961	AAB36187 AAU04197 AAV06445 AAW51088 AAB36182 AAU74192 AAW78898 AAG307319 AAG30818 AAG48818	ALIGNMENTS 286 AA. rotein. face antigen; lifiers tive signal p
73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 74 61.9 74 41.9 74 41.9 74 41.9 74 41.9 75 74 70.0 75 75 75 75 75 75 75 75 75 75 75 75 75 7	22 22 22 20 20 20 20 20 20 20 20 20 20 2	222 222 222 223 223 223 223 223 223 223	in; ; ; A2 pr surf country putat
73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 73 69.5 74 61.9 74 41.9 74 41.9 74 41.9 74 41.9 75 74 70.0 75 75 75 75 75 75 75 75 75 75 75 75 75 7	276 280 280 288 288 278 278 276 278	2288 2288 2288 2288 2288 2288 2288 228	i; Prote rst entr ensis VS. variable cocation, l25 /note= "  NWO-US19
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	26 5 4 4 3 2 5 4 4 3 2 5 6 5 6 5 6 5 6 5 6 5 6 6 6 6 6 6 6 6	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	092; P-1992; Chia homol homol accin chia chia r. 1999

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                                                                                                                          Enrilchia chaffeenist. Its maino acid sequence was deduced from a partial open reading frame (ORF2) of a genomic locus (see AAV07179) of E. chaffeenist that was obtained on the basis of homology to the major antigenic protein Mapl (see AAW51088) of Cowdria ruminantium. This genomic locus included 5 ORFs encoding similar, but non-identical proteins (see AAW51081-95). A claimed composition comprises a nucleic acid (see AAW51091-95). A claimed composition cysee AAW51089-99) that elicits a protective immune response against a rickettsial pathogen. The nucleic acid is used, in human or veterinary medicine, in vaccines to protect against Rickettsia, Ehrlichia, haplasma and Cowdria species. The Ehrlichia antigenic polypeptides can be used diagnostically to detect antibodies protein a infection (claimed).
               Composition containing nucleic acid encoding rickettsial antigen - useful for, e.g. stimulating protective immune response in humans or
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30;
                                                                                                              This is the full-length variable surface antigen VSA2 protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 286;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 105; DB 19; 100.0%; Pred. No. 1.7e-08; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY06946 standard; Protein; 286 AA.
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                                                                               Claim 3; Fig 2A; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E. chafeensis OMP-1D protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0059353.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ehrlichia chafeensis.
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N-PSDB; AAX34746.
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Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                286 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    detection; dog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                              animals
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The present sequence shows a high degree of similarity to the major antigenic protein 1 (MAP1) of Ehrlichia sp. The MAP1 gene may be used in a vaccines to protein animals or humans against rickettsial diseases caused by a organisms of Rickettsia sp., Ehrlichia sp., Anaplasma sp. or Cowdria sp. The vaccine elicits an immune response protective against the rickettsial pathogen. The nucleic acid vaccines can be driven by the human cytomegalovirus (HGWV) enhancer-promoter. Owdria ruminatium genes designated map 2, Ihworf3, 4hworf1, 18hworf1 and 3gdorf3 may be used in therapeutic and diagnostic applications. The oplypeptides are useful for detecting antibodies associated with infection by a rickettsial pathogen whilst the polynuclectides may be used to detect the presence of rickettsial nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides useful as DNA vaccines for conferring immunity to rickettsial infection e.g. heartwater caused by Cowdria ruminantium, comprises major antigenic protein 1 or 2 gene of rickettsial pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McGuire TC;
consist of proteins shown in AAY06959-970. The proteins and genes are used to detect {\rm E}_{\cdot} chaffeensis in patients and {\rm E}_{\cdot} canis in dogs.
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          Ehrlichia chaffeensis; VSA2; variable surface antigen 2; MAP1; and or antigenic protein 1; antirickettsial; vaccine; gene therapy; Rickettsia; Cowdria; Anaplasma; map2; Ihworf3; 4hworf1; 18hworf1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barbet AF, Bowie MV, Ganta RR, Burridge MJ, Mahan SM, McGuire
Rurangirwa FR, Moreland AL, Simbi BH, Whitmire WW, Alleman AR;
                                                                                                                                      0;
                                                                                                    Length 286;
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                                                                                                                                      Indels
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Pred. No. 1.7e-08;
                                                                                                    Score 105; DB 20;
Pred. No. 1.7e-08;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                          Ehrlichia chaffeensis partial VSA2.
                                                                                                                                                                                                                                                                                          AAB36186 standard; Protein; 286 AA.
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                                                                                                                                      ;
                                                                                                    100.0%;
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                                                                                                                                                                       1 NTTVGVFGIEQDWDRCVIS 19
                                                                                                                                                                                         (first entry)
                                                                                                    Query Match
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ehrlichia chaffeensis,
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N-PSDB; AACÉ8703.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                         02-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-NOV-2000
                                                     Seguence
                                                                                                                                                                                                                                                                                                                         AAB36186;
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                                                                                                                                                                                                                                                          RESULT
AAB36186
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Matches

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AAU04196 RESULT

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This is the full-length variable surface antigen VSA4 protein of Enlichia chaffensis. Its amino acid sequence was deduced from a partial open reading frame (ORF4) of a genomic locus (see AAV07179) of E. chaffeensis that was Obtained on the basis of homology to the major antigenic protein MAP1 (see AAW51088) of Cowdria ruminantium. This genomic locus included 5 ORFs encoding similar, but non-identical protein see AAW51091-95). A claimed composition comprises a nucleic acid (see AAW51091-95). A claimed composition (see AAW51089-99) that elicits a protective immune response against a rickettsial pathogen. The nucleic acid is used, in human or veterinary medicine, in vaccines to protect against Rickettsia, Enlichia, Anaplasma and Cowdria species. The Ehrlichia antigenic polypeptides can be used diagnostically to detect antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Composition containing nucleic acid encoding rickettsial antigen - useful for, e.g. stimulating protective immune response in humans or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.3%; Score 77; DB 19; Length 280; 68.4%; Pred. No. 0.00037; ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                        MAP1 homologue; variable surface antigen; VSA4; rickettsia;
                                                                                                                                                                                                                                                                                                                                                                                                                         1..25 /note= "putative signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ganta RR, Mahan SM,
                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                    Ehrlichia chaffeensis VSA4 protein.
      AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB36188 standard; Protein; 280 AA.
AAW51094 standard; Protein; 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Fig 2B; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-US19044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0733230.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||:|||||::|||| ||
60 nttigvfglkqdwdgstis 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burridge MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barbet AF, Burridge MJ
Nyika A, Rurangirwa FR;
                                                                                                                                                                                                                                                                                                                               Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYFL ) UNIV FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-251232/22.
N-PSDB; AAV07179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9816554-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-0CT-1996;
                                                                                                                      14-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-APR-1998.
                                                              AAW51094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          animals
                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
AAB36188
                                                                                                                                                                                                                                                                                                                                                                                                 Key
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      NAME OF COLOR OF STATES AND STATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New MAP2 genes and polypeptides useful as vaccines for conferring immunity to human and animal rickettsial diseases, e.g. heartwater, or as molecular markers in nucleic acid analysis procedures
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Major antigenic protein 1; MAP1; vaccine; immunogenic; rickettsia; infection; heartwater; diagnostic; variable surface antigen; VSA.
   .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Variable surface antigen 2 (VSA2) from Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nyika A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barbet AF, Ganta RR, McGuire TC, Burridge MJ, Rurangirwa FR, Mahan SM, Bowie MV, Alleman AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 105; DB 22;
Pred. No. 1.7e-08;
; Mismatches 0;
;
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Fig 2A-2B; 30pp; English
                                                                                                                                                                                                                                                                 AAU04196 standard; Protein; 286 AA.
0
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100.0%;
                                                       97US-0953326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-0733230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.

Best Local Similarity 100.

Matches 19; Conservative
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ehrlichia chaffeensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYFL ) UNIV FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-424487/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-0CT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-0CT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US6251872-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUN-2001
19;
                                                                                                                                                                                                                                                                                                                               AAU04196;
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McGuire TC;

ó;

Gaps

; 0

02-MAR-2001 (first entry)

AAB36188;

XX

RESULT AAW51094

δλ q Nyika A;

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The sequence represents the amino acid sequence of variable surface has similarity to major antigen broitein (MAP). The MAP polynucleotides and polypeptides are useful as vaccines for conferring immunity to rickettsia infection, including Cowdia man markers in muncleic acid amalysis procedures, and to produce the MAP polynucleotides may be used as molecular markers in nucleic acid analysis procedures, and to produce the MAP polypeptides, which may be used to raise antibodies that are reactive with the polypeptides. The nucleic acids may further be used as probes to identify complementary sequences within other nucleic acid molecules or genomes, where such probes can be applied to identify or distinguish infectious strains of organisms in diagnostic procedures or in rickettsial research where identification of particular organisms or strains is
                                                                                                                                                                                                                                                                                                                                      New MAP2 genes and polypeptides useful as vaccines for conferring immunity to human and animal rickettsial diseases, e.g. heartwater, or as molecular markers in nucleic acid analysis procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 77; DB 22; Length 280;
Pred. No. 0.00037;
3; Mismatches 3; Indels
                                                                                                                                                                                                              McGuire TC, Burridge MJ,
SM, Bowie MV, Alleman AR;
                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Fig 2A-2B; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY06948 standard; Protein; 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E. chafeensis OMP-1F protein.
                                                                                97US-0953326.
                                                                                                                          96US-0733230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0059353.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 68.4 les 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||:||||:||||
nttigvfglkqdwdgstis
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                                                                                                                                                                                                              Barbet AF, Ganta RR,
Rurangirwa FR, Mahan
                                                                                                                                                                    (UYFL ) UNIV FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ehrlichia chafeensis.
                                                                                                                                                                                                                                                                          WPI; 2001-424487/45.
N-PSDB; AAS07578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection; dog
US6251872-B1.
                                                                              17-OCT-1997;
                                                                                                                          17-0CT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-1999
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                                       26-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY06948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      needed.
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Matches
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Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence shows a high degree of similarity to the major antiganic protein 1 (MAPI) of Ehrlichia sp. The MAPI gene may be used in a vaccines to protect animals or humans against rickettsial diseases caused by a organism of Rickettsia sp., Ehrlichia sp., Anaplasma sp. or Cowdria sp. The vaccine elicits an immune response protective against the rickettsial pathogen. The nucleic acid vaccines can be driven by the human cytomegalovirus (HGNV) enhancer-promoter. Cowdria ruminatium genes designated map 2, Ihworf3, 4hworf1, 18hworf1 and 3gdorf3 may be used in therapeutic and diagnostic applications. The applyeptides are useful for detecting antibodies associated with infection by a rickettsial pathogen whilst the polynoclectides may be used to detect the presence of rickettsial nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides useful as DNA vaccines for conferring immunity to rickettsial infection e.g. heartwater caused by Cowdria ruminantium, comprises major antigenic protein 1 or 2 gene of rickettsial pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                          Barbet AF, Bowle MV, Ganta RR, Burridge MJ, Mahan SM, McGuire TC;
Rurangirwa FR, Moreland AL, Simbi BH, Whitmire WW, Alleman AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                      Bhrlichia chaffeensis; VSA4; variable surface antigen 4; MAPI; and and and and antigenic protein 1; antirickettsia!, vaccine; gene therapy; Rickettsia; Cowdria; Anaplasma; map2; Ihworf3; 4hworf1; 18hworf1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Major antigenic protein; MAP; vaccine; immunogenic; rickettsia; infection; heartwater; diagnostic; variable surface antigen; VSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Variable surface antigen 4 (VSA4) from Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 77; DB 21; Le
Pred. No. 0.00037;
3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU04198 standard; Protein; 280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 45-46; 63pp; English.
                  Ehrlichia chaffeensis partial VSA4
                                                                                                                                                                                                                                                                                                 21-APR-2000; 2000WO-US10886.
                                                                                                                                                                                                                                                                                                                                         99US-0130725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NTTVGVFGIEQDWDRCVIS 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 73.3
Best Local Similarity 68.4
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |||:||||:|||| ||
60 nttigvfglkqdwdgstis
                                                                                                                                                                 Ehrlichia chaffeensis:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ehrlichia chaffeensis
                                                                                                                                                                                                                                                                                                                                                                                  UYFL ) UNIV FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-679675/66.
N-PSDB; AAC68705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 AA;
                                                                                                                                                                                                         WO200065063-A2.
                                                                                                                                                                                                                                                                                                                                         22-APR-1999;
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Sequence

AAU04198;

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RESULT AAU04198

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Gaps

; 0

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Gaps

; 0

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Composition containing nucleic acid encoding rickettsial antigenuseful for, e.g. stimulating protective immune response in humans or \ensuremath{\mathsf{useful}}
                                                                                                                                                                                                                                                                                                                                                                                                                                  MAP1 homologue; variable surface antigen; VSA5; rickettsia;
                                        Score 73; DB 20; Length 256; Pred. No. 0.0014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McGuire TC;
                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                            Ehrlichia chaffeensis VSA5 protein (partial sequence).
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/note= "putative signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      associated with Ehrlichia infection (claimed)
                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ganta RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                    AA.
                                                                                                                                                                                                                                                                    AAW51095 standard; Protein; 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Fig 2B; 39pp; English.
                                          69.5%;
68.4%;
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                                                                                                                         1 NTTVGVFGIEQDWDRCVIS 19
                                                                                                                                                 96US-0733230
                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nyika A, Rurangirwa FR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ehrlichia chaffeensis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-251232/22.
                                          Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-0CT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-0CT-1996;
                                                                                                                                                                                                                                                                                                                                                   14-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barbet AF,
                                                                                                                                                                                                                                                                                                             AAW51095;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                            10
                                                                                                                                                                                                                                                 AAW51095
                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                       The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in AAXV6943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAXV6959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1. -1(B to Z) shown in AAV06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAV06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel outer membrane proteins from Ehrlichia chaffeensis and
                                                                                                                       membrane proteins from Ehrlichia chaffeensis and
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 74; DB 20; Length 280;
Pred. No. 0.0011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY06942 standard; Protein; 256 AA.
                                                                                                                                                                                   Claim 16; Fig 8B; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 18; Fig 1; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                70.5%;
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60 ntttgvfglkgdwdgstis 78
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                   Rikihisa Y;
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                                                         WPI; 1999-254290/21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                      280 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256 AA;
                                                                               N-PSDB; AAX34748
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                                                                                                                     Novel outer memk
Ehrlichia canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ehrlichia canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detection; dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9913720-A1
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                   Ohashi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY06942;
                                                                                                                                                                                                                                                                                                                                                                         Sequence
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Matches
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δλ
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This is the near full-length variable surface antigen VSA5 protein of Ehrlichia chaffeensis; it lacks about 5-7 C-terminal amino acid residues. The VSA5 amino acid sequence was deduced from a partial open reading frame (ORF5) of a genomic locus (see AAV07179) of E. chaffeensis that was obtained on the basis of homology to the major antigenic protein MAP1 (see AAW51089) of Cowdria ruminantium. This genomic locus included 5 ORFs encoding similar, but non-identical proteins (see AAW51091-95). A claimed composition comprises a nucleic acid (see AAW07176-82) encoding a polypeptide (see AAW51088-99) that elicits a protective immune response against a rickettsial pathogen. The nucleic acid is used, in human or veterinary medicine, in vaccines to protect against Rickettsial, Ehrlichia, madicine, in vaccines to protect against Rickettsial, Ehrlichia, polypeptides can be used diagnostically to detect antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 276;
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Pred. No. 0.0015;
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68.4%;
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Best Local Similarity
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9

Matches

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AAB36189

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The sequence represents the amino acid sequence of variable surface antigen 5 (VSA5) isolated from Entlichia chaffeensis, which has similarity to major antigen protein (MAP). The MAP polynucleotides and polypeptides are useful as vaccines for conferring immunity to ricettistal infection, including Cowdria ruminantium causing heartwater. The MAP polynucleotides may be used as molecular markers in nucleic analysis procedures, and to produce the MAP polypeptides, which may be used to raise antibodies that are reactive with the polypeptides. The nucleic acids may further be used as probes to identify or genomes, where such probes can be applied to identify or distinguish infectious strains of organisms in diagnostic procedures or in ricketsial research where identification of particular organisms or strains is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New MAP2 genes and polypeptides useful as vaccines for conferring immunity to human and animal rickettsial diseases, e.g. heartwater, as molecular markers in nucleic acid analysis procedures
                                                                                                                                                                                   Major antigenic protein; MAP; vaccine; immunogenic; rickettsia; infection; heartwater; diagnostic; variable surface antigen; VSA
                                                                                                                                          Variable surface antigen 5 (VSA5) from Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ehrlichia chaffeensis major antigenic protein 1 (MAP1).
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Alleman AR;
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68.4%; Pred. No. 0.0015;
iive 3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barbet AF, Ganta RR, McGuire TC, B
Rurangirwa FR, Mahan SM, Bowie MV,
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                       AAU04199 standard; Protein; 276 AA.
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                                                                                                     (first entry)
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N-PSDB; AAS07578.
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es 13; Conserv
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                                                                                                                                                                                                                                                                                                                        26-JUN-2001.
                                                                                                  23-OCT-2001
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                                                              AAU04199;
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Matches
AAW51089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence shows a high degree of similarity to the major antigenic protein 1 (MPL) of Ehrlichia sp. The MAPI gene may be used in a vaccinin 1 (MPL) of Ehrlichia sp. The MAPI gene may be diseases caused by a organism of Rickettsial sp., Ehrlichia sp., Anaplasma sp. or Cowdria sp. The vaccine elicits an immune response protective against the rickettsial pathogen. The nucleic acid vaccines can be driven by the human cytomegalovirus (HCMV) enhancer promoter. Cowdria ruminatium genes designated map 2, ihworf3, Hworf1, Bhworf1 and 3gdorf3 may be used in therapeutic and diagnostic applications. The polypeptides are useful for detecting antibodies associated with used to detect the presence of rickettsial nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides useful as DNA vaccines for conferring immunity to rickettsial infection e.g. heartwater caused by Cowdria runianatium, comprises major antigenic protein 1 or 2 gene of rickettsial pathogens
  Gaps
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                                                                                                                                                                                                                                                                                                                                    Ehrlichia chaffeensis; VSA5; variable surface antigen 5; MAP1; antidor antigenic protein 1; antirickettsial; vaccine; gene therapy; Rickettsia; Cowdria; Anaplasma; map2; 1hworf3; 4hworf1; 18hworf1; 3gdorf3.
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    Indels
  3;
Mismatches
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                                                                                                                                                                                                                                                                                                 Ehrlichia chaffeensis partial VSA5
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3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-APR-2000; 2000WO-US10886.
                                       1 NTTVGVFGIEQDWDRCVIS 19
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Conservative
                                                              Ehrlichia chaffeensis.
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Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAC68706
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                                                                                                                                                                                                                                                          02-MAR-2001
13;
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                                                                                                                                                                                                                     AAB36189;
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Nyika A;

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Gaps

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Indels

RESULT 12

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Length 276;

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N-PSDB; AAS07576.
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22-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-0CT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUN-2001.
                                                                             Barbet AF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU04193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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  NAME OF THE PART O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ehrlichia chaffeensis; MAP1; major antigenic protein 1; antirickettsial; vaccine; gene therapy; Rickettsia; Cowdria; Anaplasma; map2; 1hworf3; 4hworf1; 18hworf1; 3gdorf3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This polypeptide comprises the major antigen protein 1 gene (MAP1) of Ehrlichia chaffeensis. It is encoded by the MAP1 gene (see AAV07177). A claimed composition comprises a nucleic acid (see AAV07176-82) encoding a polypeptide (see AAW51088-99) that elicits a protective immune response against a rickettsial pathogen. The nucleic acid is used, in human or veterinary medicine, in vaccines to protect against Rickettsia, Ehrlichia, Anaplasma and Cowdia species. The nucleic acid does not replicate in the host but remains episomal and capable of expressing polypeptide for at least 19 mth. The Ehrlichia antigenic polypeptides can be used diagnostically to detect antibodies associated with Ehrlichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    Composition containing nucleic acid encoding rickettsial antigen - useful for, e.g. stimulating protective immune response in humans or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
MAP1 gene; major antigenic protein 1; rickettsia; DNA vaccine.
                                                                                                                                                                                                                                                                                 McGuire TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 73; DB 19; Length 280; Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                               Mahan SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                               Ganta RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 18-19; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB36183 standard; Protein; 280 AA.
                                                                                                                                                            97WO-US19044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.5%;
                                                                                                                                                                                                96US-0733230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-APR-2000; 2000WO-US10886.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NTTVGVFGIEQDWDRCVIS 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ehrlichia chaffeensis MAP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                               Burridge MJ,
                                                                                                                                                                                                                                                                                                    Nyika A, Rurangirwa FR;
                                     Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ehrlichia chaffeensis
                                                                                                                                                                                                                                       (UYFL ) UNIV FLORIDA
                                                                                                                                                                                                                                                                                                                                        WPI; 1998-251232/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infection (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 AA;
                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAV07177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200065063-A2
                                                                                                                                                          17-0CT-1997;
                                                                                                                                                                                                17-OCT-1996;
                                                                           WO9816554-A1
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                                                                                                                  23-APR-1998
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                                                                                                                                                                                                                                                                             Barbet AF,
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The present sequence is given in a specification relating to nucleic acid vaccines containing genes to protect animals or humans against rickettsial diseases caused by a organisms of Rickettsia sp., Ehrlichia Sp., Anaplasma sp. or Cowdria sp. The vaccine elicits an immune response protective against the rickettsial pathogen. The vaccine comprises the major antigenic protein 1 (MAP1) gene or the major antigenic protein 2 (MAP2) gene of rickettsial pathogens. The nucleic acid vaccines can be driven by the human cytomegalovirus (HCMV) enhancer-promoter. Cowdria ruminatium genes designated map 2, lhworf3, 4hworf1, 18hworf1 and 3ddorf3 may be used in therapeutic and diagnostic applications. The polypeptides are useful for detecting antibodies associated with infection by a rickettsial pathogen whilst the polynucleotides may be used to detect the presence of rickettsial nucleic acids.
                                                                                                                                                                                                                                                                                                                         New polynucleotides useful as DNA vaccines for conferring immunity to rickettsial infection e.g. heartwater caused by Cowdria ruminantium, comprises major antigenic protein 1 or 2 gene of rickettsial pathogens
                                                                                                                                 McGuire TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                             Ganta RR, Burridge MJ, Mahan SM, McGuire
nd AL, Simbi BH, Whitmire WW, Alleman AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Major antigenic protein 1; MAP1; vaccine; immunogenic; rickettsia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nyika A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burridge MJ,
, Alleman AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 73; DB 21;
Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barbet AF, Ganta RR, McGuire TC, B
Rurangirwa FR, Mahan SM, Bowie MV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 35-36; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU04193 standard; Protein; 280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection; heartwater; diagnostic.
                                                                                                                                                                   Rurangirwa FR, Moreland AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.5%;
68.4%;
99US-0130725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NTTVGVFGIEQDWDRCVIS 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 69.5
Best Local Similarity 68.4
Matches 13; Conservative
                                                                                                                                 Bowie MV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ehrlichia chaffeensis
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                                                                (UYFL ) UNIV FLORIDA
                                                                                                                                                                                                                             WPI; 2000-679675/66.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280 AA;
                                                                                                                                                                                                                                                               N-PSDB; AAC68700
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New MAP2 genes and polypeptides useful as vaccines for conferring immunity to human and animal rickettsial diseases, e.g. heartwater, or as molecular markers in nucleic acid analysis procedures

Disclosure; Column 15-17; 30pp; English.

The sequence represents the amino acid sequence of major antigenic protein 1 (MAPI) from Ehrlichia chaffeensis. The MAP polynucleotides and holypeptides are useful as vaccines for conferring immunity to rickettsia infection, including Cowdria ruminantium causing heartwater. The MAP polynucleotides may be used as molecular markers in nucleic acid analysis procedures, and to produce the MAP polypeptides, which may be used to raise antibodies that are reactive with the polypeptides. The nucleic acids may further be used as probes to identify or complementary sequences within other nucleic acid molecules or genomes, where such probes can be applied to identify or distinguish infectious strains of organisms in diagnostic procedures or in rickettsial 

Sequence 280 AA;

Query Match 69.5%; Score 73; DB 22; Length 280; Best Local Similarity 68.4%; Pred. No. 0.0015; Matches 13; Conservative 3; Mismatches 3; Indels

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Gaps ; 0

1 NTTVGVFGIEODWDRCVIS 19 ||||||||||::|:|| || 60 nttvgvfglkqnwdgsais 78

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Search completed: March 14, 2002, 09:09:38 Job time: 429 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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1 NPTVALYGLKQDWEGISS 18
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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	Description		COZIO ENLICHIA C	052104 ehrlichia c	085357 ehrlichia c	Q9rh35 ehrlichia c	085817 ehrlichia c	052107 ehrlichia c	09zqj2 ehrlichia c	085358 ehrlichia c		Q9amf6 cowdria sp.		Q9adv3 ehrlichia c	Q46327 cowdria rum	Q9afal cowdria rum	O85816 ehrlichia c	Q9zqm9 ehrlichia c	Q9r8a9 ehrlichia c	Q9r8a8 ehrlichia c	Q9r8a7 ehrlichia c
	ΠD		007700	052104	085357	Q9RH35	085817	052107	Q92GJ2	085358	Q9ACI9	Q9AMF6	Q9F473	Q9ADV3	046327	Q9AFA1	085816	Q92GM9	Q9R8A9	Q9R8A8	Q9R8A7
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æ	Query	1 0 0 0 6	7007	90.7	63.8	8.09	8.09	8.09	8.09	59.8	59.8	57.7	57.7	57.7	57.7	57.7	55.7	55.7	54.6	54.6	54.6
	Score		7	88	62	29	59	59	59	28	28	99	26	26	26	26	54	54	53	53	53
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1 NPTVALYGLKQDWEGISS 18

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Ogr8a6 ehrlichia c Ogr8a5 ehrlichia c Ogr3j3 ehrlichia c Ogr472 ehrlichia c Ogr472 ehrlichia c Ogr491 ehrlichia c Ogr492 cowdria rum Ogs6h1 cowdria rum Ogs6h1 cowdria rum Ogs6h2 cowdria rum Ogr425 cowdria rum Ogr433 cowdria rum Ogr433 cowdria rum Ogr633 cowdria rum Ogr634 cowdria rum Ogr634 cowdria rum Ogr475 ehrlichia c	AA. e update) ion update) ion; Rickettsiales; teins of Ehrlichia chaffeensis amily."; ahan S.M., Burridge M.J., surface antigen gene family of 43(1998).	; Length 278; .08; indels 0; Gaps 0;
2 09R8A6 2 09R8A5 2 09R343 2 09F472 2 09F472 2 09AF99 2 09AF98 2 09AF98 2 046330 2 046330 2 046330 2 046330 2 046330 2 09AF98 2 09F474 3 09F476 5 09F476	PRT; 278 AA.  Created) Last sequence upor Last annotation of the subdivision; Ehrlichia.  PRT; 278 AA.  Created) Last annotation of the subdivision; Ehrlichia.  PRT; 278 AA.  Rathisa Y.;  Rikihisa Y.;  Rikihisa Y.;  Rikihisa Y.;  Rembrane protein;  C multigene famil.  (998).  A47746;  Barbet A.F., Mahan  of a 28 kDa surfenun. 247:636-643(19:	100.0%; Score 97; DB 2 100.0%; Pred. No. 7.8e- ive 0; Mismatches
54.6 54.6 54.6 54.6 54.6 54.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.7 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6 53.6	PRELIMIN  R (TrEMBLE  (TRE	th 100 Similarity 100 18; Conservative
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SEQUENCE FROM N.A.
SERVINCENT;
MEDLINE-99175287; PubMed-10074538;
MEDLINE-99175287; PubMed-10074538;
Yu X.J., MCBride J.W., Walker D.H.;
Yu X.J., MCBrided J.W., Walker D.H.;
"Genetic diversity of the 28-kilodalton outer membrane protein gene in human isolates of Ehrlichia chaffeensis.";
"Genetic AF077735; AAC31548.1;
InterPro; IPR001702; Gram_neg_porin.
InterPro; IPR001702; Surface_A9_msp4.
Prints: PR00181; Surface_A9_msp4.
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Bacteria: Proteobacteria: alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
NCBI_TaxID=945;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-UNOV-1998 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
00TER MEMBRANE PROTEIN P28 PRECURSOR.
Ehrlichia chaffeensis.
Ehrlichia chaffeensis.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae, Ehrlichiaee; Ehrlichia.
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                                                                                                                                                            Length 280;
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Yu X.-J., Walker D.H.;
"Ebrilchia chaffeensis 28 kDa outer membrane protein.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL. AF077734: AAC31547.1;
EMBL. AF0777751: AAC31547.1;
EMBL. AF077771: Surface_A9_msp4.
Pfam: PF01017: Surface_A9_2.1.
SEQUENCE 276 AA: 30027 MW; 2FD3698FCFIF60BE CRC64;
        Surface_Ag_2; 1.
AA; 30743 MW; FBB841DAF08EE4DC CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2001 (TrEMBLrel. 17, Last annotation update)
01-UNY-2001 (TREMBLREL. 17, Last annotation update)
00TER MEMBRANE_PROTEIN P28 PRECURSOR (FRAGMENT).
                                                                                                                                                            Score 62; DB 2;
Pred. No. 0.038;
4; Mismatches
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60 NTTIGVFGLKQDWDG 74
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29 NTTAGVEGLKQDWDG 43
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    Pfam; PF01617;
SEQUENCE 280
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Hochem. Blophys. Res. Commun. 247:636-643(1998).
EMBL: ARCO2971.1;
InterPro; IPR002566; Surface_Ag_msp4.
Pfam, PF01617; Surface_Ag_2; 1. -
SEQUENCE 280 AA, 30322 MM; BD835E491086DF01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98084465; PubMed-9423849; Ohashi N., Zhi N., Zhang Y., Rikihisa Y.; Immunodominant major outer membrane proteins of Ehrlichia chaffeensis are encoded by a polymorphic multigene family."; Infect. Immun. 66:132-139(1998).
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SEQUENCE FROM N.A.
STRAIN-ARKANSAS;
MEDLINE-98321180; PubMed-9647746;
Acddy G.R., Sulsona C.R., Barbet A.F., Mahan S.M., Burridge M.J.,
Alleman A.R.;
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Rickettsiaceae; Ehrlichieae; Ehrlichia.
NCBI_TaxID=945;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
28 KDA MAJOR SURRACE ANTIGEN-4.
Ehrlichia chaffeensis.
Bacteria: Proteobacteria: alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichiaee; Ehrlichiae.
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llarity 83.3%; Pred No. 2.3e-06;

Conservative 2; Mismatches 1; Indels
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
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0MP-IC (28 KDA MAJOR SURFACE ANTIGEN-1).
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MEDLINE=98321180; PubMed=9647746;
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Ehrlichia chaffeensis.
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Matches 15; Conserv
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McBride J.W., Yu, Xj, Walker D.H.; "Molecular cloning of the gene for a conserved major immunoreactive 28-kilodalton protein of Ehrlichia canis: a potential serodiagnostic
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                                                                                                            P SUDCENCE.
C STRAIN—JAKE;

X MEDLINE-20432107; PubMed=10974556;
X MCBride J.W., YU X.J., Walker D.H.;
XT "A conserved, transcriptionally active p28 multigene locus of RT aconserved, transcriptionally active p28 multigene locus of RT Ehrlichia canis.";
RL Gene 254:245-252(2000).
DR EMBL; AF078553; AAC68667.1; -.
DR EMBL; AF0785744; AAG144362.1; -.
DR FMBL; AF0787745; Surface_A9_msp4.
DR Pfam; PF01617; Surface_A9_2: 1.
SEQUENCE 288 AA; 31590 MW; 86DCAECB88E9BF5E CRC64;
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MEDLINE-98321180; PubMed=9647746;
Reddy Gr., Sulsona C.R., Barbet A.F., Mahan S.M., Burridge M.J.,
Alleman A.R.;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-UNOV-1998 (TrEMBLrel. 08, Last sequence update)
20.501 (TrEMBLrel. 17, Last annotation update)
28 KDA MAJOR SURFACE ANTIGEN-5 (FRACMENT).
28 KDA MAJOR SURFACE ANTIGEN-5 (FRACMENT).
Bacteria: Proteobacteria: alpha subdivision; Rickettsiales;
Rickettsiaceae; Enrlichieae; Ehrlichia.
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EMBL; AF062761; AAC26716.1; ...
InterPro; IPR002566; Surface—Ag_msp4.
Pfam; PF01617; Surface—Ag_2; 1.
NON TER 276 276
SEQUENCE 276 AA; 29782 MW; A9AB2A92263CA4EA C
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MEDLINE=99242757; PubMed=10225842;
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Best Local Similarity 60.0
Matches 9; Conservative
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NTTTGVFGLKQDWDG 74
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NTTVGVFGLKQNWDG 73
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"Immunodominant major outer membrane proteins of Ehrlichia chaffeensis are encoded by a polymorphic multigene family.";
Infect. Immun. 66:132-139(1998).
EMBL: U72291; AAC02940.1;
InterProt. IPRO02566; Surface_Ag_msp4.
Pfam; PF01617; Surface_Ag_ms p4.
SEQUENCE 280 AA; 30731 MW; CCAA6C34E2AF393E CRC64;
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                                                                                                                                                                                                                                                                                                   Ehrlichia chaffeensis.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
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Rickettslaceae; Ehrlichieae; Ehrlichia.
                            Length 276;
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
30-KDA MAJOR OUTER MEMBRANE PROTEIN (P28-8).
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Last annotation update)
                            Score 59; DB 2;
Pred. No. 0.12;
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Pred. No. 0.12;
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MEDLINE=98084465; PubMed=9423849;
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Best Local Similarity 60.0%;
Matches 9; Conservative
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01-JUN-1998 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                       1 NPTVALYGLKQDWEG 15
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59 NTTAGVFGLKQDWDG 73
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60 NTTTGVFGLKQDWDG 74
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SEQUENCE FROM N.A.
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                                           Local Similarity
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SEQUENCE FROM N.A.
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01-JUN-1998 (
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MEDITAGE 99242757; PubMed-10225842; MEDITAGE 99242757; PubMed-1025842; MCDITAGE 1W. Yu. Xi, Walker D.H.; MOJecular cloning of the gene for a conserved major immunoreactive 28-kilodalton protein of Ehrlichia canis: a potential serodiagnostic
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MDDLINE-21153566; PubMed-11254561;
Ohashi N., Rikihisa Y., Unver A.;
Ohashi N., Rikihisa Y., Unver A.;
"Analysis of Transcriptionally Active Gene Clusters of Major Outer Membrane Protein Multigene Family in Ehrlichia canis and E. chaffeensis.";
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Enrlichia canis.
Bacteria, Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceee; Ehrlichieae; Ehrlichia.
NCBI_TaxID=944;
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STRAIN-OKLAHOWA;
MEDLINE-98371112;
Ohashi N., Unver A., Zhi N., Rikihisa Y.;
Cloning and characterization of multigenes encoding the immunodominant 30 Kilodalton major outer membrane proteins charlichia canis and application of the recombinant protein:
Serodiagnosis.,
J. Clin. Microbiol. 36:2671-2680(1998).
                                                                                                                                                   Ehrlichia canis.
Bacteria: Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae: Ehrlichieae; Ehrlichia.
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MUBLINE=20132107; PubMed-10974556;
MCBLINE=20132107; PubMed-10974556;
MCBRIGGO, TW. YU X.J., Walker D.H.;
A conserved, transcriptionally active p28 multigene locus
Ehrlichia canis.";
Ehrlichia canis.";
EMBL; A45-222(2000).
EMBL; A6022744; AAG44361.1; -.
InterPro; IPR002566; Surface_Aq_msp4.
ERM; PR002566; Surface_Aq_msp4.
ERM; PR00151; Surface_Aq_2.1;
ERGUENCE 280 AA; 30762 WW; BE284A4B94FE3123 CRC64;
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Llarity 60.0%; Pred. No. 0.36;
Conservative 2; Mismatches 4; Indels
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MAJOR OUTER MEMBRANE PROPERT P30-2.
                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-010-2001 (TrEMBLrel. 17, Last annotation update)
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Best Local Similarity
Matches 9; Conserv
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STRAIN-ARKANSAS;
MEDLINE-98084465; PubMed=9423849;
Ohashi N., Zhang Y., Rikihisa Y.;
"Immunodominant major outer membrane proteins of Ehrlichia chaffeensis are encoded by a polymorphic multigene family.";
Infect. Immun. 66:132-139(1998).
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MEDLINE=21153566; PubMed=11254561;
Ohashi N., Rikihisa Y., Unver A.;
"Analysis of Transcriptionally Active Gene Clusters of Major Outer
Membrane Protein Multigene Family in Ehrlichia canis and E.
chaffeensis.";
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Bacteria, Proteobacteria, alpha subdivision; Rickettsiales; Rickettsiaceae; Ehrlichieae; Cowdria.
                                                          Ehrlichia chaffeensis.
Bacteria: proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
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Allscopp M.T., Allscopp B.A.;
An oovel Birlichia detected in dogs in South Africa.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF325175;
ARK14320.1; -.
NON_TER 272
SEQUENCE 273
SEQUENCE 
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EMBL. 072291; AAK286731; -.
SEQUENCE. 281 AA, 30343 WW; A99ESF7C4459AA9A CRC64;
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-UN-2001 (TrEMBLrel. 17, Last sequence update)
01.-UN-2001 (TrEMBLrel. 17, Last annotation update)
MAJOR ANTIGENIC PROTEIN MAP1 (FRAGMENT).
01-JUN-2001 (TrEMBLrel. 17, Last annotation update) MAJOR OUTER MEMBRANE PROTEIN P28.
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Pred. No. 0.35;
5; Mismatches
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50.0%;
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Best Local Similarity 60.0
Matches 9; Conservative
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Bensaid A., Maillard J.-C., Chantal I., Perez J.-M., Martinez D.;
"Cowdria runninantium major antigenic protein 1 (map1) gene variants
are not geographically constrained.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF355200; AAK27216.1;
SEQUENCE 284 AA: 30720 MW; B0D3AEB9F9AB09C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-SENEGAL STOCK;
MEDLINE-94178956; PubMed-8132352;
van Vliet A.H., Jongelan F., van Kleef M., Van der Zeijst B.A.;
Nolecular cloning, sequence analysis, and expression of the gene encoding the immunodominant 32-kilodalton protein of Cowdria ruminantium.";
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Rickettsiaceae; Ehrlichieae; Cowdria.
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Rickettsiaceae; Ehrlichieae; Cowdria.
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EMBL; X74250; CAA5309.1; -
InterPro; IPRO02566; Surface_Ag_msp4.

Brain: PFO1617; Surface_Ag_22; 1.

SEQUENCE 284 AA; 30634 MW; 53228A889D28BEB8 CRC64;
Infect. Immun. 69:2083-2091(2001).
EMBL; AF078553; AAK28699.1; -.
SEQUENCE 280 AA; 30803 MW; 27238BEIC7E68A91 CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 10, Last annotation update)
01-JUN-2001 (TrEMBLREL. 17, Last annotation update)
01-JUN-2001 (TrEMBLREL PROTEIN P28 PRECURSOR.
Ehrlichia chaffensis.'
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.7%; Score 54; DB 2; Length 280;
61.5%; Pred. No. 0.76;
tive 3; Mismatches 2; Indels
Score 56; DB 2; Length 284;
Pred. No. 0.37;
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"Ehrlichia chaffeensis 28 kDa outer membrane protein.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AR07732; ARC31545.1; -.
InterPro: IRR002566; Surface_Ag_msp4.
Pfam; PF01617; Surface_Ag_2; 1.
SEQUENCE 280 AA; 30277 WW; 91C54AC78507A63F CRC64;
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Title: Perfect score: Sequence:

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100059 seqs, 36664827 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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CYP4_HUMAN FINC_CANFA	FINC_HORSE PPCM_HUMAN	PLO3_HUMAN	FINC_MOUSE	VGLD_HSV2	FUCP_HAEIN	AGP4_HUMAN	CDGT_BACOH	ADB2_YEAST
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## ALIGNMENTS

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Structural and chemical properties of a flavodoxin from Anabaena PCC
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Fillat M.F., Borrias W.E., Weisbeek P.J.;
"Isolation and overspression in Escherichia coli of the flavodoxin
gene from Anabaena PCC 7119.";
Biochem. J. 280:187-191(1991).
                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POLY-ARG.
POLY-GLU.
POLY-GLU.
POLY-GLN.
N-LINKED (GLCNAC. .) (POTENTIAL).
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MEDLINE-88296496; PubMed=2500643;
MEDLINE-88296496; Straus N.A.;
Leonhardt K.G., Straus N.A.;
"Sequence of the flavodoxin gene from Anabaena variabilis 7120.";
Nucleic Acids Res. 17:4384-4384(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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Pred. No. 39;
1; Mismatches 4; Indels
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Anabaena sp. (strain PCC 7119).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690; 1168;
                              POTENTIAL.
EXTRACELLULAR (POTENTIAL).
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01-NOV-1990 (Rel. 16, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
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STRAIN-PCC 7119;
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Fillat M.F., Edmondson D.E., Gomez
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Burkhart B.M., Ramakrishnan B., Yan H., Reedstrom R.J., Markley J.L.,
Straus N.A., Sundaralingam M.;
Structure of the trigonal form of recombinant oxidized flavodoxin
from Anabaena 7120 at 1.40-A resolution.";
Acta Crystallogr. D 51:318-330(1995).
7. RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
STRAIN-PCC 7119;
MEDLINE-99318886; pubmed=10388575;
Fernandez-Recio J., Romero A., Sancho J.;
"Energetics of a hydrogen bond (charged and neutral) and of a
cation-pi interaction in apofilavodoxin.";
J. Mol. Biol. 290:319-330(1999).
-- FUNCTION: LOW-POTENTIAL ELECTRON DONOR TO A NUMBER OF REDOX
                                                                                                  "Hydrogen-1, carbon-13, and nitrogen-15 NMR spectroscopy of Anabaena 7120 flavodoxin: assignment of beta-sheet and flavin binding site resonances and analysis of protein-flavin interactions."; Biochemistry 29:9600-9609(1990).
                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
STRAIN=PCC 7120;
MEDLINE-93271891; PubMed=1303762;
Rao S.T., Shaffie F., Yu C., Satyshur K.A., Stockman B.J.,
Markley J.L., Sundaralingam M.; Satyshur from Anabaena 7120
"Structure of the oxidized long-chain flavodoxin from Anabaena 7120
Protein Sci. 1:1413-1427(1992).
Stockman B.J., Krezel A.M., Markley J.L., Leonhardt K.G.,
Straus N.A.;
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PR EMBL: X14577; CAA32720.1;

PR: S04600: S04600.

PR: S1374; S1374.

PR: S20298; S20298.

PR: PBB; IFFUV; 31-0CT-93.

PR: PBB; IFFG; 25-DEC-96.

PR: PBB; IFFG; 20-MAY-99.

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-!- COFACTOR: FMN.
-!- SIMILARITY: BELONGS TO THE FLAVODOXIN FAMILY.
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SETAILA-ATCC 29145 / SP7;
MEDLINE=94186025; PubMed=8138139;
Zimmer W., Hundeshagen B.;
Zimmer W., Hundeshagen Grant W., Hunder W.,
Zimmer W., Hundeshagen W., Mandine B. A.
Zimmer W., The Gatase Domain Belong To Type-1 Glutamine
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;
Azospirillum.
                                                                                                                                                                                                                                                                                                                            4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S25101; S25101.
InterPro; IPR000991; GATase_1.
Pfam: PF00117; GATase_1.VPE_1: 1.
PROSTIE: PS00442; GATASE_TYPE_1: 1.
Pyrimidine biosynthesis; Ligase; Glutamine amidotransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.3%; Score 41; DB 1; Length 544;
                                                                                                                                                                                                                                                                                  1; Length 452;
                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                             Tuberculist; Rv2097c; -
Hypothetical protein; Complete proteome.
SEQUENCE 452 AA; 51384 MW; 12AF8B7872D2F5EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13AA1A8B8EB6C5DB CRC64;
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(BY SIMILARITY).
(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            544 AA
                                                                                                                                                                                                                                                                                  ch 42.3%; Score 41; DB 1. Similarity 47.6%; Pred. No. 25; 10; Conservative 1; Mismatches
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516 GZ
518 GZ
59908 MW;
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                                                                                                                     EMBL; Z73966; CAA98209.1; -. EMBL; AE007065; AAK46439.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Azospirillum brasilense.
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                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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518
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PYRG_AZOBR
                                                                                                                                                                                                                                                                                                                                                                                                       161
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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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-!- SIMILARITY: TO RHODOCOCCUS STRAIN N186/21 HYPOTHETICAL PROTEIN IN
THCR 5'REGION (ORF6) (AC P43484).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98295987; pubMed-9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmaier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Lociphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Whole genome comparison of Mycobacterium tuberculosis clinical and
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                          BBOBBDOBGDEF9A58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
8.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROTHETICAL 51.4 KDA PROTEIN RV2097C.
RV2097C OR MT2158 OR MTCY49.37C.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                          18832 MW;
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Best Local Similarity
Matches 8; Conserv
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SEQUENCE FROM N.A.
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Q10706;
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P10340;
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PIR; $131277; $23127;
PIR; $131277; $13127;
PIR; $131277; $13127;
PIRO00623; Shik_kinase_I.
InterPro: IPR002097; Shik_mate_DH.
Pfam; PF01487; DHquinase_I; 1.
Pfam; PF01488; Shikimate_DH; 1.
Pfam; PF01202; SKI; 1.
Ouinate metabolism; Transcription regulation; Repressor; DNA-binding.
SEQUENCE 918 AA; 100580 MW; 67EDA399CBF098B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Geever R.F., Huter L., Baum J.A., Tyler B.M., Patel V.B.,
Rutledge B.J., Case M.E., Giles N.H.;
Nourospora crassa."
J. Mol. Biol. 207:15-34(1989).
J. Mol. Biol. 207:15-34(1989).
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                            Gaps
                            ;
                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
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66.7%; Pred. No. 52;
iive 0; Mismatches 4; Indels
                            Indels
                            5,
                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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Last annotation update)
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  Pred. No. 30;
1; Mismatches
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                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=74-OR23-1A;
MEDLINE-89293848; Pubmed=2525625;
                                                                                                                                                                                                                                                                                    01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequ
01-0CT-1981 (Rel. 17, Last anno
0UINATE REPRESSOR.
04-15.
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Llarity 53.8%;
Conservative
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                                                                                                                      410 NPVVGLLGLMTEW 422
                                                                      1 NPTVALYGLKQDW 13
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  Best Local Similarity
Matches 7; Conserv
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                          RESULT 5
OAIS_NEUCR
DAIS_NEUCR
DT 01-067-1989
DE CUINATE REPLOY
CC BUKARYOCOR F RO STRAIN-4-0R
RX MEDLINE-8929
RA GEOVER R.F. TO STRAIN-4-0R
RX MEDLINE-8929
RA GEOVER R.F. TO STRAIN-14-0R
RX MEDLINE-8929
RA GEOVER R.F. TO STRAIN-14-0R
RY MEDLINE-81277
DR INTERPRO! IP
DR PFAM: PF0148
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DHP1_SC
ID DH
AC P4
AC P4
DT 01
DT 20
DT 20
DE P1
GN DE P1
OS SC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; S43891; S43891.
Nuclear protein: Hydrolase; Nuclease; Exonuclease.
DOMAIN 264 268 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
SEQUENCE 991 AA: 112367 MW; 83FA34D93DADADOO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-972.

STRAIN-972.

MCLEan J., Harris D., Barrell B.G., Rajandream M.A., Walsh S.V.;

MCLEan J., Harris D., Barrell B.G., Rajandream M.A., Walsh S.V.;

Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: ESSENTIAL FOR VEGETATIVE CELL GROWTH. CAN BIND TO DNA

AND HAS.5'-3' EXORIBONUCLEASE ACTIVITY.

-!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).

-!- SIMILARITY: TO YEAST RATI; SOME, TO YEAST KEMI/DST2 AND S.POMBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 1-29.
SEQUENCE FROM N.A., AND SEQUENCE OF 1-29.
STRAIN=975;
MEDIINE=94347347; PubMed=8190062;
MEDIINE=9447347; PubMed=8190062;
MOJECULIAR analysis of the dhp1+ gene of Schizosaccharomyces pombe: an essential gene that has homology to the DST2 and RATI genes of Saccharomyces cerevisiae.
MOJ. Gen. Genet. 243:1-8(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ٥.
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MEDLINE-81216115; PubMed=6406674;
Smith W.W., Pattridge K.A., Ludwig M.L., Petsko G.A., Tsernoglou
Tanaka M., Yasunobu K.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ő
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

BEDILINE-B8086879; Pubmed-3121586;
Laudenbach D.E., Reith M.E., Straus N.A.;
"Isolation, sequence analysis, and transcriptional studies (Ilavodoxin) gene from Anacystis nidulans R2.";
J. Bacteriol. 170:258-265(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41; DB 1; Length 991;
Pred. No. 56;
5; Mismatches 5; Indels
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces. Schizosaccharomyces. NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-1989 (Rel. 10, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
FLAYODOXIN.
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706 NFTIDLNGKKFEWQGVA 722
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Best Local Similarity 41.2
Matches 7; Conservative
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EMBL; M59757; AAA21273.1; -.
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Best Local Similarity
--Loc 8; Conserva
                                                                                                                         169 AA;
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                                                                                                                                                                                                                                                                                                                     Bacillus subtilis.
                                                                                                                                                                                                                                                 DCOP_BACSU
P25971;
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                                                            "Refined structures of oxidized flavodoxin from Anacystis nidulans."; J. Mol. Biol. 294:711-724(1999).
                                          Drennan C.L., Pattridge K.A., Weber C.H., Metzger A.L., Hoover D.M.,
                                                                                              MEDLINE-20079530; PubMed-10610792; Hoover D.M., Drennan C.L., Metzger A.L., Osborne C., Weber C.H., Pattrigge K.A., Ludwig M.L.; Comparisons of wild-type and mutant flavodoxins from Anacystis nidulans. Structural determinants of the redox potentials."; J. Mol. Biol. 294:725-743(1999).
                                                                                                                                                                                            Anacystis nidulans with 3D'NMR.";
Biochemistry 30:7718-7730(1991).
-!- FUNCTION: LOW-POTENTIAL ELECTRON DONOR TO A NUMBER OF REDOX
                                                                                                                                                         STRUCTURE BY NMR.
MEDLINE=91329335; PubMed=1907844;
Clubb R.T., Thanabal V., Osborne C., Wagner G.;
"IH and 15N resonance assignments of oxidized flavodoxin from
"Structure of oxidized flavodoxin from Anacystis nidulans."; J. Mol. Biol. 165:737-755(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Electron transport; Flavoprotein; FMN; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C -> S (IN REF. 2).
FG -> GF (IN REF. 2).
                                                                                                                                                                                                                             -!- COFACTOR: FMN.
-!- INDUCTION: BY IRON-STRESS.
-!- SIMILARITY: BELONGS TO THE FLAVODOXIN FAMILY.
                                                                                     X-RAY CRYSTALLOGRAPHY (1.86 ANGSTROMS).
                         X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
                                   MEDLINE=20079529; PubMed=10610791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001226; Flavodoxin.
Pfam; PF00258; flavodoxin; 1.
PROSITE; PS00201; FLAVODOXIN; 1.
                                                                                                                                                                                                                                                                                                                                       EMBL; M19116; AAA22050.1; -.
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168
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1CZH; 29-DEC-99.
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A28670; A28670.
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167
                                                   Ludwig M.L.;
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1D03;
1D04;
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                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i - CATALYTIC ACTIVITY: OROTIDINE-5'-PHOSPHATE = UMP + CO(2).
-i - PATHARY: SIXTH AND LAST STEP IN THE BIOSYNTHESIS OF PYRIMIDINES.
-i - SUBUNIT: HOMODIMER.
-i - SIMILARITY: BELONGS TO THE OMP DECARBOXYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pyrimidine biosynthesis; Lyase; Decarboxylase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIANCE-91225016; PubMed-1709162;
Quinn C.L., Stephenson B.T., Switzer R.L.;
Functional organization and nucleotide sequence of the Bacillus subtilis pyrimidine biosynthetic operon.";
J. Biol. Chem. 266:9113-9127(1991).
                                                                                                                                                               ;
                                                                                                1; Length 169;
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                                                                                                                                                               5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
0ROTIDINE 5'-PHOSPHATE DECARBOXYLASE (EC 4.1.1.23) (OMP
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DB1743714ED052E7 CRC64;
18646 MW; CF049E12F9C6AA1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=1423;
                                                                                  DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 AA
                                                                                                                                                               Mismatches
                                                                                            Score 40;
Pred. No.
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PROSITE; PS00156; OMPDECASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; 299112; CAB13429.1; -. PIR; 139845; 139845. Subtilist; BG10719; pyrF. InterPro; 1PR001754; OMPdecase.
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SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
Herrmann R.;
"Complete sequence analysis of the genome of the bacterium Mycoplasma"
             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales;
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                                                                                                                                                                                                Mycoplasma pneumoniae.
Bacteria; Firmloutes; Bacillus/Clostridium group; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL 75.4 KDA PROTEIN IN AUT1-CSE2 INTERGENIC REGION.
YNROOBW OR N2042.
                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 24:4420-4449(1996).
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
STRONG, TO M.GENITALIUM MG335.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 41.2%; Score 40; DB 1; Length 341; Best Local Similarity 75.0%; Pred. No. 27; Indels Matches 6; Conservative 1; Mismatches 1; Indels
             7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE000034; AAB96007.1; -.
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2: 1.
Hypothetical protein; Transferase; Glycosyltransferase; Complete proteome.
SEQUENCE 341 AA; 40414 MW; C209F50D714CB3D0 CRC64;
                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MG-2001 (Rel. 40, Last annotation update)
HYPOTHEICAL PROTEIN MG335.2 HOMOLOG (P01_ORF341).
MPN483 OR MP359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    661 AA.
Pred. No. 18;
1; Mismatches
                                                   222 DPVKAYKAVRLEWEGIKS 239
                                   1 NPTVALYGLKQDWEGISS 18
Best Local Similarity 38.9
Matches 7; Conservative
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SEQUENCE FROM N.A.
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26 LKQDWNGV 33
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                                                                                                                                                                                                                                                                                                                              pneumoniae."
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P40345;
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                                                                                           TEAST
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STRAIN=S288C / FY1679;
MEDLINE=95208356; PubMed=7900425;
Verhasselt P., Aert R., Voet M., Volckaert G.;
"Twelve open reading frames revealed in the 23.6 kb segment flanking the centromere on the Saccharomyces cerevisiae chromosome XIV right arm.";
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM
                                                                                                                                                                                               Yeast 10:1355-1361(1994).
-!- SIMILARITY: SOME, TO MAMMALIAN PHOSPHATIDYLCHOLINE-STEROL O-ACYLTRANSFERASE.
-!- SIMILARITY: TO S.POMBE SPBC776.14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
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Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 35.7%; Pred. No. 54;
Matches 10; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL 01C043319A836F44 CRC64;
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PRB., S45131; S45131.
PR., S45131; S45131.
SGD: S0005291; YNR008W.
InterProx: IPR003386; LACT.
Pfan; PF02450; LACT; 1.
Hypothetical protein; Transmembrane.
TRANSMEM 81 101
SEQUENCE 661 AA, 75393 MW, 01C04331.
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389 TLAMYGLEKFFSRIERVKMLQTWGGIPS 416
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NCBI_TaxID=542;
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MEDIATION: ELECTRECALLY SILENY TRANSPORTER SYSTEM WHICH IS A MEDIATOR OF SODIUM AND CHLORIDE REABSORPITON. PLAYS A VITAL ROLE IN THE REGULATION OF IONIC BALANCE AND CELL VOLUME.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-!- SIMILARITY: BELONGS TO THE SIC12A FAMILY OF TRANSPORTERS.
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                             Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Sphingiodea; Sphingidae; Sphinginae; Manduca.
                                                                                                                      ;
                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
BUMETANIDE-SENSITIVE SODIUM-(POTASSIUM)-CHLORIDE COTRANSPORTER
                                                                                               Length 734;
                                                                                                                      Indels
        EMBL; AF213822; AAF23789.1; -.
InterPro; IPR000728; AIRS_related.
Pfam; PF00586; AIRS; 2.
Putine blosynthesis; Ligase; ATP-binding.
NP_BIND 106 117 ATP (POTENTIAL).
SEQUENCE 734 AA; 77679 MW; B771635E0F66A166 CRC64;
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EXTRACELLULAR (POTENTIAL)
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POTENTIAL.
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DOMAIN 1 122 CYTOPLASMIC (POTENTIAL).
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                                                                                                DB 1;
60;
                                                                                                                                                                                                                       PRT; 1060 AA
                                                                                                                     Mismatches
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IPR002027; Amino_acid_permease.
IPR002443; NaKCl_trnsportr
                                                                                                Score 40;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Malpighian tubules;
MEDLINE=96035837; Pubmed=7550244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00324; aa_permeases; 1.
PRINTS; PR01207; NAKCLTRNSPRT.
                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
                                                                                                41.2%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U17344; AAA75600.1; -.
                                                                                                                      Conservative
                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122
143
153
174
197
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249
270
275
296
3331
                                                                                                                                                      2 PTVALYGLKQDW 13
                                                                                                                                                                                                                                                                                      (NA-K-CL SYMPORTER).
                                                                                              Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            276
297
332
                                                                                                                                                                                                                                                                                                                                                                                                  Reagan J.D.;
                                                                                                                                                                                                                                                    01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                     NKCL_MANSE
Q25479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
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DOMAIN
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                                                                                                                                                                                                  RESULT
CC DR KW KW SO PR SO FT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ## PECALITY NOTE SET TO BE A SECONDERS OF STATEMENT OF STATEMENT OF STATEMENT REAL MEDICAGE STATEMENT RNA HELICAGE NUCLEAR EXPORT OF SPLICED MRNA BY RELEASING THE SPLICED MRNA BY RELEASING THE SPLICED SOME."; Genes Dev. 10:997-1007(1996).

-: FUNCTION: FACTLITATES NUCLEAR EXPORT OF SPLICED MRNA BY RELEASING THE RNA FROM THE SPLICEDSOME.
-: SUBCELLUIAR LOCATION: NUCLEAR A NUCLEAR LOCALIZATION SIGNAL, AND APPEARS TO FACILITATE THE INTERACTION WITH THE SPLICEDSOME.
-: SIMILARITY: BELONGS TO THE "DEAD" BOX FAMILY HELICASE. DEAH SUBPAMILY: DDX8/PRP22 ORTHOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-95021291; PubMed=7935475;
Ono Y., Ohno M., Shimura Y.;
"Identification of a putative RNA helicase (HRH1), a human homolog of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ATP-DEPENDENT HELICASE DDX8 (RNA HELICASE HRH1) (DEAH-BOX PROTEIN 8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 1; Length 1060;
Pred. No. 88;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                             4C39D1F0B645FFFF CRC64;
                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL). POTENTIAL.
                                                                                                             POTENTIAL.
EXTRACELLULAR (POTENTIAL).
                                         EXTRACELLULAR (POTENTIAL).
                                                                                         CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1220 AA.
                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . Cell. Biol. 14:7611-7620(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.2%;
                                                                                                                                                                                                                                                                                                                                                                                                117392
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 58.30,
T; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
367
388
431
452
497
497
562
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664
664
663
902
1060
396
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                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                               664
8882
903
396
404
419
816
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Q14562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yeast Prp22.
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SIMILARITY: THE GATASE DOMAIN BELONGS TO TYPE-1 GLUTAMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 40...
3, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                        AMIDOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhizobiaceae; Rhiz
NCBI_TaxID=103798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NODA_RHIS3
P72329:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
ACT_SITE
SEQUENCE
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NODA_RHIS3
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STRAIN-JAL-J, DSM 2661 / ATCC 43067;

MEDLINE-96337999; Pubmed-8686087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Bult C.J., Mite O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus

januaschii."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K->E: IN GET; INHIBITION OF PRE-MRNA
SPLICING AND NUCLEAR EXPORT OF UNSPLICED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRE-MRNA
OF UNSPLICED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   010-NOV-1997 (Rel. 35, Created)
12-DEC-1998 (Rel. 37, Last sequence update)
12-AGG-2001 (Rel. 40, Last annotation update)
12-AGG-2001 (Rel. 40, Last annotation update)
13-AGG-2001 (Rel. 40, Last annotation update)
14-AGG-2001 (Rel. 40, Last annotation update)
15-AGG-2001 (Rel. 40, Last annotation update)
15-AGG-2001 (Rel. 40, Last annotation update)
16-AGG-2001 (Rel. 40, Last annotation update)
17-AGG-2001 (Rel. 40, Last annotation update)
18-AGG-2001 (Rel. 40, Last annotation 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
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Pred. No. 1e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methanococcus jannaschii.
Archaea; Buryarchaeota; Methanococcales; Methanococcaceae;
Methanococcus.
WCBI_TaxID=2190;
EMBL, D50487; BAA09078.1; -. HISP; D65055; 1SRO.
HIMS: D600396; -. Literpro: IPR001410; DEAD.
Interpro: IPR001410; DEAD.
Interpro: IPR001464; DEALLATP_helcse.
Interpro: IPR00309; S1.
Interpro: IPR00309; S1.
Interpro: IPR00309; S1.
Interpro: IPR00309; S1.
Interpro: IPR00409; BELDC: I.
SMART; SM00409; HELICC: I.
SMART; SM00409; DEAH_ATP_HELICASE; I.
INTERPROITE: IPR0069; DEAH_ATP_HELICASE; I.
INTERPROITE: IPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNA.
S->L: IN LAT; INHIBITION OF SPLICING AND NUCLEAR EXPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17C1602A73A0EF24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 ARG/SER-RICH (RS DOMAIN).
S1 MOTIF.
ATP (POTENTIAL).
DEAH BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             354 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 41.2%;
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1220 AA; 139314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 VALYGLKQDWEGI 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
NP_BIND
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUTAGEN
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CARA_METJA
           qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhizobium sp. (strain N33).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              GLUTAMINE AMIDOTRANSFERASE.
GATASE (BY SIMILARITY).
4D8F07776CA65F9F CRC64;
                                                                                                                                                                                                                                                                                                            PRINTS; PR00096; GATASE.
PRINTS; PR00099; CPSGATASE.
PROSTIE; PS00442; GATASE_TYPE_I; FALSE_NEG.
Arginine blosynthesis; Pyrimidine blosynthesis; Ligase;
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-MUG-2001 (Rel. 40, Last annotation update)
MODICATION PROTEIN A (EC 2.3.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39.5; E
Pred. No. 34;
4; Mismatches
                                                                                                                                                                                                                Interpro: IPR001317; CPS_GATase.
InterPro: IPR002414; CPSase_sm_chain.
InterPro: IPR000991; GATase_1.
Pfam: PF00988; CPSase_sm_chain; 1.
Pfam: PF00117; GATase: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                               CPSASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 250 G
354 AA; 39920 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.78;
                                                                                                                                                        EMBL; U67544; AAB99021.1; -. HSSP; P00907; 1JDB. TIGR; MJ1019; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 PTVALYGLKQDW---EGISS 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | || :|| :|| :|| :|| 56 PLEGNYGVKKDWFESDGIKA 75
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0
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                                                                                                                                                Query Match

40.2%; Score 39; DB 1; Length 196;
Best Local Similarity 46.2%; Pred. No. 22;
Matches 6; Conservative 4; Mismatches 3; Indels
            EMBL, U53327; AAB16892.1; -.
InterPro; IPR003484; NodA.
Pfam; PF02474; NodA; 1.
PROSITE; PS01349; NODA; 1.
Transferase; Acyltransferase; Nodulation.
SEQUENCE 196 AA; 21727 MW; CA065D2046F3F061 CRC64;
                                                                                                                                                                                                               4 VALYGLKQDWEGI 16
: |||::|||:
88 IGLYGVRPDLEGL 100
CC
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Search completed: March 14, 2002, 09:24:53 Job time: 909 sec

Db

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

US-09-765-739A-6 97 Title: Perfect score:

1 NPTVALYGLKQDWEGISS 18 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 Total number of hits satisfying chosen parameters:

219241 segs, 76174552 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database :

pir1:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	28k surface antige	surface	28k surface antige	or antig	28k surface antige	28k surface antige	hypothetical prote	zin		probable nadh oxid	probable alpha-man	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	immediate-early pr	hypothetical prote	hypothetical prote	hypothetical prote	subtilisin-type pr	thiazide-sensitive	flavodoxin - Anaba	flavodoxin - Anaba	conserved hypothet	phosphoglycerate t	hypothetical prote	hypothetical prote	CTP synthase (EC 6	regulatory protein
SUMMARIES	ID	JE0216	JE0217	JE0218	140882	JE0219	JE0221	, G64558	A96533	F82084	G71838	G71133	A71950	T44301	S75205	T43979	T09313	T40131	T29345	G75073	C84120	A47296	S18374	804600	H72222	E82426	970	T15839	S25101	S04255
	Length DB							122 2																						
	Query Match Le	100.0	63.9	59.8	57.7	52.6	49.5	46.9	٠.	45.4	45.4	45.4	44.8	44.3	4	4.		•	•	43.3		•			•	•	•			
	Score	97	62	58	26	51	48	45.5			44	4	43.5	43		43	-	42.5	42	42	42	42	41	41	41			41	41	41
	Result No.	-	7	e	4	Ŋ	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

dna exoribonucleas		hypothetical prote	hypothetical prote	antirestriction pr	flavodoxin [valida	orotidine-5'-phosp	ATP-binding protei	hypothetical prote	<ul> <li>hypothetical prote</li> </ul>	probable membrane	probable aminopept	bumetanide sensiti	hypothetical prote	probable RNA helic	pre-mRNA splicing
543891	T16668	F83935	G83495	A42716	A28670	I39845	F69309	S73685	H71091	S45131	G71308	T30823	T28130	A56236	T49915
010	~	~	~	N	7	N	7	7	7	ď	~	7	7	7	~
991	180	105	135	169	170	239	254	341	374	661	774	1060	1122	1220	1226
42.3	41.8	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2
41	40.5	40	40	40	40	40	40	40	40	40	40	40	40	40	40
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 JED216 28k surface antigen 3 - Ehrlichia chaffensis 28k surface antigen 3 - Ehrlichia chaffensis 3 k surface antigen 3 - Ehrlichia chaffensis NiAlternate names: MAPI C; Species: Ehrlichia chaffensis C; Species: 1-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 17-Mar-1999 C; Accession: JED216 R; Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.B. Biochem. Biochem. Biophys. Res. Commun. 247, 636-643, 1998 A; Title: Molecular characterization of a 28kDa surface antigen gene family of the transcensesion: JED216 A; Reference number: JED216; MUID:98321180 A; Reference type: DNA A; Residues: 1-278 < RED> A; Cross-references: GB:AF062761	Query Match 100.0%; Score 97; DB 2; Length 278; Best Local Similarity 100.0%; Pred. No. 2.5e-08; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QQ δ

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Gaps ; 0 63.9%; Score 62; DB 2; Length 280; 60.0%; Pred. No. 0.014; ive 4; Mismatches 2; Indels Query Match 63.9 Best Local Similarity 60.0 Matches 9; Conservative

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1 NPTVALYGLKQDWEG 15 60 NTTIGVFGLKQDWDG 74 Óλ Ωp

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Gaps

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RESULT 7 (364558 hybotein HP0311 - Helicobacter pylori (strain 26695) (5.5pecies: Helicobacter pylori (5.4cession: 664558 (5.5pecies: Mitte, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Glodek, A.; Morke son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujil, C.; Bowman, C.; Bowman, C.; Matthey, A.; Mallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A; Reference number: A64520; MUID:97394467 A; Actaus: preliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1.122 cyroh>
A; Residues: 1.122 cyroh>
A; Residues: 1.122 cyroh>
A; Residues: 1.122 cyroh>
A; Residues: Teferences: GB:AE000549; GB:AE000511; NID:92313403; PIDN:AAD07384.1; PID:9231
                                                                                                                                                                                                                                            Sek surface antigen 2 - Ehrlichia canis
C;Species: Ehrlichia canis c;Species: Ehrlichia canis c;Species: Ehrlichia canis c;Species: Ehrlichia canis c;Species: Ehrlichia canis c;Species: Ehrlichia canis c;Species: Ehrlichia canis c;Species: Ehrlichia canis c;Species: Ehrlichia canis c;Species: Ehrlichia canis c;Species: Ehrlichia canis c;Species: Ehrlichia c;Species: Ehrlichia c;Species: Ehrlichia c;Species: Ess. Commun. 247, 636-643, 1998
Biochem. Biophys. Res. Commun. 247, 636-643, 1998
A;Title: Molecular characterization of a 28kDa surface antigen gene family of the tri A;Reference number: JE021
A;Reference number: JE021
A;Reference number: JE021
A;Residues: I-133 <RED>A;Residues: I-133 <RED>A;Cross-references: GB:AF062762; NID:g3327964; PIDN:AAC26722.1; PID:g3327966
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5;
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Pred. No. 1.3;
3; Mismatches
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Pred. No. 3;
2; Mismatches
Mismatches
5;
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ilarity 55.6%;
Conservative
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illarity 56.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 TTVVYGLKENWAGDAISS 79
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Conservative
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55 NQILAFYGLKINDWQG 70
                                                           '1 NPTVALYGLKQDWE 14
                                                                                                                      60 NTTVGVFGIEQDWD
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Matches 10; Conserv
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Best Local Similarity
Matches 9; Conserv
7;
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Matches
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                                                28k surface antigen 5 - Ehrlichia chaffensis
NiAlternate names: MAPI
C;Spacies: Ehrlichia chaffensis
C;Date: 21-Aug-1998 acquence_revision 21-Aug-1998 #text_change 17-Mar-1999
C;Accession: JE0218
R;Reddy G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Biochem. Biophys. Res. Commun. 247, 636-643, 1998
A;Title: Molecular characterization of a 28kDa surface antigen gene family of the tribe A;Reference number: JE0216; MUJD:98321180
A;Reference number: DNA
A;Reference number: DNA
A;Residues: 1-276 < RED>
A;Residues: 1-276 < RED>
A;Cross-references: GB:AF062761
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28k surface antigen 2 - Ehrlichia chaffensis
38k surface antigen 2 - Ehrlichia chaffensis
6; Decises: Ehrlichia chaffensis
6; Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 17-Mar-1999
6; Accession: JE0219
8; Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Biochem: Biophys. Res. Commun. 247, 636-643, 1998
A; Fitle: Molecular characterization of a 28kDa surface antigen gene family of the tribe
A; Reference number: JE0216; MUID:98321180
A; Recession: JE0219
A; Molecule type: DNA
A; Residues: 1-286 < RED>
A; Cross-references: GB:AF062761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               major antigenic protein - heartwater rickettsia

G.Species: Cowdraia ruminantium (heartwater rickettsia)

G.Species: Cowdraia ruminantium (heartwater rickettsia)

G.Species: Cowdraia ruminantium (heartwater rickettsia)

G.Species: Cowdrain and the sequence_revision 16-Aug-1996 #text_change 08-Oct-1999

G.Species: Cowdrain and the sequence_revision 16-Aug-1996 #text_change 08-Oct-1999

G.Species: Tablet, A.H.; Jongedjan, F.; van Kleef, M.; van der Zeijst, B.A.

A.Title: Molecular cloning, sequence analysis, and expression of the gene encoding the A.Title: Molecular cloning, sequence analysis, and expression of the gene encoding the A.Title: Molecular cloning, sequence analysis, and expression of the gene encoding the A.Scatus: preliminary; translated from GB/EMBL/DDBJ

A.Scatus: preliminary; translated from GB/EMBL/DDBJ

A.Scatus: 1-284 cRES>

A.Molecule type: DNA

A.Residues: 1-284 cRES>

G.Genetics:
A.Genetics:
A.Genetics:
A.Genetics:
A.Genetics:
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Pred. No. 0.14;
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Pred. No. 0.92;
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Pred. No. 0.06
4; Mismatches
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50.0%;
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50.0%;
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Best Local Similarity 60.0
Matches 9; Conservative
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Best Local Similarity 50.0
Matches 8; Conservative
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59 NTTVGVFGLKQNWDG 73
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Best Local Similarity
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A;Cross-references: GB:AE001545; GB:AE001439; NID:g4155776; PIDN:AAD06772.1; PID:g415 A;Experimental source: strain J99 C;Genetics: A;Genetics: A;Gene: nuoF
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NPTVALYGLK-QDW-----EGI 16
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                                                                                                                                                                                                                                                                  45.4%;
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ilarity 63.6%;
Conservative
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56.2%;
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Best Local Similarity 50.08
Matches 12; Conservative
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Best Local Similarity 56.2.
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Best Local Similarity
Matches 7; Conserv
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A;Gene: jhp0296
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A; Authors: Salzberg, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser. C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719
A; Recession: A96533
A; Accession: A96533
A; Molecule type: DNA
A; Residues: 1-1077 <STO>
A; Cross-references: GB:AE005173; NID:g10120424; PIDN:AAG13049.1; GSPDB:GN00141
A; Gene: F14J22.13
A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE004307; GB:AE003852; NID:99656934; PIDN:AAF95509.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
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A,Accession: G71838
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-328 <ARN>
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C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C;Accession: G71838
C;Accession
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Nature 406, 477-483, 2000
Affille: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID: 20406833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable 2-demethylmenaquinone 2-C-methyltransferase (EC 2.1.1.-) VC2366 [similarity]
C:Species: Vibrio cholorae
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: F82084
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36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.4%; Scor.
100.0%; Pred. No. cc.
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Pred. No. 7.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: VC2366
A;Map position: 1
C;Keywords: methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Best Local Similarity
'`^^ 6; Conserv?
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 QDWEGISS 18
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hypothetical protein jhp0296 - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variabry: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C;Accession: A71950
B;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D. F; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric paracterace number: A71800; MUD:99120557
A;Accession: A71950
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Nov-1999
C;Accession: G71133
R;Kawarabayasi, Y; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se
M.; Ohfuku, Y; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogw
DNA Res. S, 55-76, 1998
A;Tille: Complete sequence and gene organization of the genome of a hyper-thermophil.
A;Reference number: A71000; MUID:98344137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GB:AE001439; NID:g4154813; PIDN:AAD05873.1; PID:g415
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A. Residues: 1-856 < KAM>
A. Cross-references: GB. AP000003; NID:93236130; PIDN:BAA29929.1; PID:d1030872; PID:933.
A. Experimental source: strain Or3
A. Note: this accession replaces an interim accession for a sequence replaced by GenBa C. Genetics:
A. Genetics:
A.
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Length 328;
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                                                                                                               Indels
                                                                                                               3;
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Pred. No. 41;
2; Mismatches 2
     5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable alpha-mannosidase - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
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Pred. No. 6.4;
2; Mismatches
DB
15;
                                                                                                         1; Mismatches
Score 44;
Pred. No.
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| :| |||| ||:| 55 NQILAFYGLKIGDWQG 70

qq

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Pupotherical protein U19 [imported] - human herpesvirus 6
[C.Species: human herpesvirus 74319]
[C.Species: human herpesvirus 7, 1803-8063, 1999
[C.Species: human herpesvirus 6
[C.Species: hu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: U19
C;Superfamily: human herpesvirus 6 hypothetical protein U19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A) Residues: 1-389 <DOM>
A) Cross-references: EMBL:AF157706; PIDN:AAD49631.1
A) Experimental source: strain 229; variant B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                March 14, 2002, 09:10:46
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Best Local Similarity 33.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 VALYGLKODWEGISS 18
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79 MSMFGVTEEWEGASA 93
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Job time: 362 sec
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                                                                                                                                                                                                                                                                                                                C; Date: 1.2000 **Sequence_Tevision in integral of the alkaliphilic bacillus sp.

R; Takami, H; Nakasone, K; Ogasawara, N; Hirama, C.; Nakamura, Y; Masui, N; Fuji, F.

R; Takami, H; Nakasone, K; Ogasawara, N; Hirama, C.; Nakamura, Y; Masui, N; Fuji, F.

B; Takami, H; Nakasone, K; 1999

A; Title: Sequencing of three lambda clones from the genome of alkaliphilic Bacillus sp.

A; Recession: T44301

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Rocession: T44301

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Rocesion: T44301

A; Rosidues: 1-132 <ATAX

A; Residues: 1-132 <ATAX

A; Reference number: A83650; MUID: 20263314

A; References number: A83650; MUID: 20263314

A; Residues: 1-132 <ATAX

A; Residues: 1-133 <ATAX

A; Residues: 1-132 <ATAX

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A; Residues: 1-132 <ATAX

A; Residues: 1-133 <ATAX

A; Residues: 1-133 <ATAX

A; Residues: 1-134 <ATAX

A; Residues: 1-135 <ATAX

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A; Accession: S75205
A; Status: preliminary
A; Molacule type: DNA
A; Residues: 1-298 < KAN>
A; Residues: 1-298 < KAN>
A; Cross-references: EMBL:090903; GB:AB001339; NID:g1652127; PIDN:BAA17119.1; PID:g165219
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C; Superfamily: Synechocystis hypothetical protein s1r2052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein s1r2052 - Synechocystis sp. (strain PCC 6803)
A; variety: PCC 6803
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C; Accession: 375205
B; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                           C:Species: Bacillus halodurans
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 31-Dec-2000
                                                                                                                                                                           hypothetical protein BH0656 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 8.4;
1; Mismatches 2; Indels
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44.3%; Score 43; DB 2; Length 298;
Best Local Similarity 42.1%; Pred. No. 20;
Matches 8; Conservative 3; Mismatches 6; Indels
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Best Local Similarity 72.7%;
Matches 8; Conservative
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278 PTVIAYGKRISRSWSGVQS 296

2 PTVALYG--LKQDWEGISS:18

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Gaps

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Length 389; Indels

2,

Score 43; DB; Pred. No. 26; 8; Mismatches